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June 23, 2005, 10:41:47; Search time 1762.93 Seconds (without alignments) 5800.480 Million cell updates/sec
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| Cgn2 6/ptodata/2/pubpna/USO6 TWEW PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_TUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US110_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 6,	25,	12,	Sequence 875, App	Sequence 875, App	Sequence 124786,	Sequence 15, Appl	
. di	US-10-764-1	US-10-292-408-25	US-10-477-687-12	US-09-938-842A-875	US-09-938-842A-875	US-10-424-599-124786	US-10-292-408-15	
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Result

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              JOURNAL: Plant Physiol.
VOLUME: 113
VOLUME: 113
FAGES: 306-306
DATE: 1997-01-01
DATABASE ACCESSION NUMBER: genbank/X94938
DATABASE ENTRY DATE: 1998-02-13
RELEVANT RESIDUES: (1). (1636)
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                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 1636; Conservative
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US-10-764-138-6
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Best Local Similarity 77.4%; Pred. No. 8.6e-134;
Matches 889; Conservative 0; Mismatches 260; Indels
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APPLICANT: Feldmann, Kenneth A.
APPLICANT: Tax, Frans
ITILE OF INVENTION: DWF12 and Mutants Thereof
FILE REFERENCE: 11696-075US1
CURRENT APPLICATION NUMBER: US/10/477,687
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: PCT/US02/15563
PRIOR APPLICATION NUMBER: US 60/291,342
PRIOR FILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-05-16
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1490
                                                                                                                                                                                                                                                                                                              US-10-477-687-12
; Sequence 12, Application US/10477687; Publication No. US20050049397A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                     47.4%; Score 775.2; DB 16; Length 1744; 79.4%; Pred. No. 4.9e-142; ive 0; Mismatches 238; Indels 0;
                                                                                                   Best Local Similarity 79.4
Matches 918; Conservative
; LENGTH: 1744
; TYPE: DNA
; ORGANISM: Glycine max
US-10-292-408-25
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              60/300,111
; PRIOR APPLICATION NUMBER: US 60/31; PRIOR FILING DATE: 2001-06-22; NUMBER OF SEQ ID NOS: 5379; SEQ ID NO 875; LENGTH: 1143; TYPE: DNA APPLICATION A ORGANISM: A TABLICADE US-09-938-842A-875
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Best Local S:
Matches 885
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US-09-398-842A-875

i Sequence 875, Application US/09938842A

i Patent No. US20020160378A1

i GENERAL INFORMATION:

i APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

i APPLICANT: Wang, Xun

i APPLICANT: Wang, Xun

i TILE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

CURRENT FILING DATE: 2001-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16
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              TGAGAGCTTGTATCGAGTTCTGAAACATTATAGTAGTGCAAACCAAAGAATGCCTCTTGT
                                                                              CTATGTCAAACTTTACACATACCAAATCTTCAGAGGCTTGGCTTATATCCCATACTGCTCC
                                                                                                                         TGGTGTCTGCCACAGAGATATAAAACCACAAAATCTTTTGGTTGATCCCCACACCCATCA
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosalic David K
APPLICANT: Kovalic David K
APPLICANT: Applicant and Yahua
APPLICANT: Cao Yongwai
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
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                                             GTTAAACTTTACATGTATCAGATCTTCCGGGGACTTGCTTACATTCACAATGTTGCTGGA
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                                                                                                           GTCAAACTTTACACATACCAAATCTTCAGAGGCTTGGCTTATATCCATACTGCTCCTGGT
                                                                                                                                                                     GTCTGCCACAGAGATATAAAACCACAAAATCTTTTGGTTGATCCCCACACCATCAGTGT
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US-10-424-599-124786
; Sequence 124786, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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Publication No. US20040009476A9

GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: APPLICANT: Wang Xun
APPLICANT: APPLICANT: Wang Xun
APPLICANT: APPLICANT: Wang Xun
APPLICANT: APPLICANT: Alw, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND WETHODS OF USE
THE REPERBENCE: SCRIP130G-34

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
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                          GCATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCACAGGGCTCGAAGCTTGTGCA
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44.7%; Score 730.8; DB 11;
Best Local Similarity 77.5%; Pred. No. 2.1e-133;
Matches 885; Conservative 0; Mismatches 257;
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US-09-938-842A-875
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Sequence 15, Application US/10292408

Sequence 15, Application US/10292408

Publication No. US2030182692A1

GENERAL INFORMATION:

APPLICANT: VAN THIELEN, NOCHA

APPLICANT: DA COSTA E SILVA, OSWALDO

APPLICANT: TILE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS

TITLE OF INVENTION: OF USE IN PLANTS

TITLE OF INVENTION: OF USE IN PLANTS

TITLE OF INVENTION: OF USE IN PLANTS

CURRENT APPLICATION NUMBER: 60/346,096

PRIOR PLING DATE: 2002-11-12

PRIOR PLING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 51

SOFTWARE: Patentin Ver. 2.1

SEM-MULL 167
                                                                                                                                                                                        AATGGCCGACCTCTACCACCGTTGTTCAACTTCAAACAAGAGTTGTCTGGGGCTTCACCG 1205
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                                                                                                                                                   CTCGAGGCATGTGCGCATCCGTTTTTCAATGAACTCCGTGAGCCCAAATGCTCGTCTTCCA
                                           GAAGCCATTGACCTTGCATCTCGGCTTCTTCAATACTCACCAAGTCTACGTTGCACTGCG
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Best Local Similarity 76.6%;
Matches 868; Conservative
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CORGANISM: Brassica napus
US-10-292-408-15
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                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_83691C.1
US-10-424-599-124786
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 124786
LENGTH: 2519
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.3%;
Matches 907; Conservative
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ORGANISM: Glycine max
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413 ATCTCTTTGAAGCATTGTTTCTTTTCCACTACAAGTACTGAAGCTTTTTCTTAATTTG
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                                                            Gaps
                                     Length 1881;
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0
                                    Score 708.6; DB 18; Length
Pred. No. 5.8e-129;
0; Mismatches 264; Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32405C.1
US-10-424-599-67987
                                    Query Match 43.3%;
Best Local Similarity 76.7%;
Matches 867; Conservative
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US-10-424-599-67987
US-10-424-599-67987
Sequence 67997, Application US/10424599
Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: Las Rosa Thomas J
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Dants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 138-21 (13222) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 67987
LENGTH: 1881
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                                                AATCTTCAGAGGCTTGGCTTATATCCATACTGCTCCTGGTGTCTGCCACAGAGATATAAA
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RESULT 10
US-10-424-599-67990
US-10-424-599-67990

Sequence 67990, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Devick K

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 67990

LENGTH: 1979
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43.2%; Score 707; DB 18;
Best Local Similarity 76.6%; Pred. No. 1.2e-128;
Matches 866; Conservative 0; Mismatches 265;
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Sequence 12807, Application WS/2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Application No. Store E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)8

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NOS: 73128
    1073 ACTGCACTTGAAGCATGTGCACATCCTTTCATGAAGTTCGTGAACCCAACGCTCGC 1132
                                           CTTCCAAATGGCCGACCTCTACCACGTTGTTCAACTTCAAACAAGAGTTGTCTGGGGGCT 1199
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US-10-425-114-12807
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Matches 866; Conservative
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RESULT 11
US-10-292-408-21

i Sequence 21, Application US/10292408

i Publication No. US20030182692A1

i GENERAL INFORMATION:

APPLICANT: VAN THILEIN, NOCHA

APPLICANT: VAN THILEIN, NOCHA

APPLICANT: OF COSTA E SILVA, OSWALDO

TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS

TITLE OF INVENTION: OF USE IN PLANTS

FILE REFERENCE: 16313-0178

CURRENT FILING DATE: 2002-11-12

PRIOR APPLICATION NUMBER: 05/13/6,096

PRIOR APPLICATION NUMBER: 60/346,096

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PatentIn Ver. 2.1 ö 435 218 278 615 338 GCTTGGAGACTGGCGAGGCGAGTGGCTATAAGAAGGTCTTGCAGGACAGGCGATACAAAA 398 436 GITICITCICIACAACGACTAGAGAIGAGCTCTTCCTCAATCTCGTTAIGGAGTAIGTAC 495 578 675 698 758 795 818 GTTACATGGCCGAACGTGTTGTTGGAACAGGATCATTCGGAATTGTATTCCAGGCAAAAT GITACATGGCCGAACGTGTTGTTGCCACTGGATCATTTGGCATTGTTTTCCAGGCGAAGT creacaccarcrrccererraraaaccacracagraccarcaaacacagaarecceraa 136 CCGATATAGACAACGACAAGGAAATGTCTGCTGCTGTTATAGAAGGAAATGATGTGTATA CCGGTCACATAATTTCTACTACAATTGGAGGCAAAAATGGTGAACCTAAACAGACCATTA GCTTGGAAACTGGAGAATCAGTAGCCATTAAGAAGGTTTTGCAAGATCGCCGTTATAAAA ACCGAGAGTTGCAATTAATGCGACTAATGGACCATCCAAATGTGGTTTCCTTGAAGCATT CAGAGACATTGTACCGGGTTTTTGAAGCACTATACTAGTTCAAACCAGCGGATGCCTATCT 539 CAGGAATCTGCCATAGGGATTTGAAGCCTCAAAATCTTTTGGTTGATCGACTCACACC CTGGTGTCTGCCACAGAGATATAAAACCACAAAATCTTTTGGTTGATCCCCACACCCATC AGTGTAAGCTCTGTGATTTTTGGAAGTGCAAAAGTACTGGTGAAAGGTGAACCAAACATAT 599 AAGTCAAGCTCTGTGATTTTGGGAGTGCAAAAGTTCTGGTGGAGGGTGAATCAAACATTT CATATATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGCCACAGAGTATA Gaps ö Length 1499; Score 705; DB 16; Length 1 Pred. No. 2.7e-128; 0; Mismatches 255; Indels Query Match
Best Local Similarity 77.1%;
Matches 858; Conservative

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GCTTGGAGACTGGCGAGGCGAGTGCCTATAAAGAAGGTCTTGCAGGACAGGCGGTACAAAA
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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US-10-424-599-26109
US-10-424-599-26109
i bublication No. US20040031072A1
sequence 26109, Application US/10424599
i publication No. US20040031072A1
sequence 26109, Application No. US20040031072A1
i GENERAL INFORMATION:
    APPLICANT: La Rosa Thomas J
    APPLICANT: Cao Vongweil
    TILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
    TILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TILE REFERENCE: 38-21(53223) B
    CURRENT FILING DATE: 2003-04-28
    NUMBER OF SEQ ID NOS: 285684
    SEQ ID NO 26109
    LENGTH: 1553
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                                CAACTICTGTIGATATTIGGTCCGCTGGTTGTGTCCTTGCGGAACTICTTCTAGGCCAGC
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Best Local Similarity 77.1%; Pred. No. 2.7e-128;
Matches 858; Conservative 0; Mismatches 255; Indels
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US-10-424-599-26109
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ORGANISM: Glycine max
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APPLICANT: La Rosa: Thomas J.
APPLICANT: La Rovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Goo, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brokarok, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5)3221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ. ID NOS: 204966
SEQ. ID NO 98579
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                                                                     923 GAATCCCAACTACACAGAATTCAGATTACAGATTAAAGCTCACCCATGGCACAAGAT
                                                                                                                                                              TTTCCACAAGCGGATGCCTCCGGAAGCCATTGACCTTGCATCTCGGCTTCTTCAATACTC
                                                                                                                                                                                                 TTTCCACAAGCGGATGCCTCCAGAAGCAATTGACCTTGCATCACGTCTTCTCCAGTATGC
                                                                                                                                                                                                                                                                                       ACCAAGTCTACGTTGCACTGCGCTCGAGGCATGTGCGCATCCGTTTTTTCAATGAACTCCG
                                                                                                                                                                                                                                                                                                                          743 AGAACCCCACGCAAGGTTGCCAAATGGACGTCCATTCCCCCCACTGTTCAACTTTAAGGA
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Pred. No. 2.8e-125;
0; Mismatches 232;
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US-10-437-963-98579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 98579, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity 78.1%;
Matches 829; Conservative
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ORGANISM: Oryza Bativa
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APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 29872
LENGTH: 1922
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Pred. No. 3.9e-126;
0; Mismatches 243; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: Clone ID: PAT_MRT4530_34331C.1
US-10-437-963-29872
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Best Local Similarity 77.6%;
Matches 840; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Oryza sativa
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                                                                                                                                                            Length 1744;
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                                                                                                                                                              DB 18;
                                                                                                                                                         Score 689.2; DB 18;
Pred. No. 3.6e-125;
0; Mismatches 278;
                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_32407C.1 US-10-424-599-67989
                                                                                                                                                            Query Match
Best Local Similarity 75.7%;
Matches 867; Conservative
                                                max
LENGTH: 1744
TYPE: DNA
ORGANISM: Glycine m
FEATURE:
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Publication No. US20040031072A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILE CONTROL C
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US-10-424-599-67989
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Search completed: June 24, 2005, 08:33:13 Job time: 1766.93 secs PAGE BLANK (USPTO)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June 23, 2005, 10:16:02; Search time 8124.57 Seconds (without alignments) 7664.793 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

Scoring table:

34239544 seqs, 19032134700 residues IDENTITY NUC Gapop 10.0 , Gapoxt 1.0 Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST: \* Database :

9b est1: 9b est2: 9b est3: 9b est4: 9b est6: 9b gs81: 9b gs81: 4.6.2.....

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description.	, , , , , , , , , , , , , , , , , , , ,	CB971865 CAB10006 BX823861 Arabidops AY108486 Zea mays CX286429 BS7749151
SUMMARIES	CNSOABFT CNSOAB1V AV782577 AV782577 AV782577 AV78258 BP56058 BP560678 AV7822185 AV103545 AV103545 AV103545 AV103545 CV290871 CL964803 CV290871 CL964803 CV290871 CL964803 CV290871	CB971865 CNS0A4PT AY108486 CK286429
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## ALIGNMENTS

RESULT 1

CNSOABET LOCUS DEFINITION	
ACCESSION VERSION KEYWORDS SOURCE	GSLTLS51ZG09 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress). BX815323. BX815321. GI:42471412 HTC; GSLT_CDNA. Arabidopsis thaliana (thale cress)
ORGANISM REFERENCE AUTHORS	Arabidopsis thaliana Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1409) Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J., and Salanoubat,M.
TITLE JOURNAL AUTHORS TITLE	and 'Full-Length' cDN nd Improve Arabidopsie
JOURNAL	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage BP 191 91006 EVNY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr) The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., URGV INRA : Clepet C., Caboche M.
FEATURES SOUTCE	Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length  Thtp://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis. Location/Qualifiers 1. 1409 /organism="Arabidopsis thaliana" /mol.type="mRNA" /strain="Col-0" /db_xref="taxon:3702"

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(thale cress).
BX817800
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           tissue"
                                                                                   Score 949.4; DB 3;
Pred. No. 4.7e-181;
                                                                                             Pred. No. 4.7e-181;
0; Mismatches 161;
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1. .1409
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                                              /gene="At1g06390"
                                                                                   Query Match
Best Local Similarity 86.4%;
Matches 1062; Conservative
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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

Bp 191 91006 EWRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Cleptet C., Cabone M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Wunich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
Little: Www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSOABIV 11461 bp mRNA linear HTC 06-FEB-200-
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTSIL42ZC04 of Silique of strain col-0 of Arabidopsis thaliana
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales; Brassicaceae, Arabidopsis.
GATGTATGAACCCGAACTACACAGATTTTAGGTTCCCACAAATCAAAGCTCACCCTTGGC 975
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Location/Qualifiers
                                                                            ATAAGGTTTTCCACAAGCGGATGCCTCCGGAAGCCATTGACCTTGCATCTCGGCTTCTTC
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    1. 1461
    /organism="Arabidopsis thaliana"

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Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-3159
Fax: 81-298-36-3159
Fax: 81-298-36-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a Sstl/Khol insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.
                                                                                                                                    GCCCGACCTCTACCACCGTTGTTCAACTTCAAACAAGAGTTGTCTGGGGCTTCACCGGAG 1208
                                                                                                                                                                                                                                      AV782577
AV782577 RAFL4 Arabidopsis thaliana cDNA clone RAFL04-19-E04 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 709)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Arakawa,T., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y., and Shinozaki,K.
                                                                                                                                                                                                                                                                                              CTTATCAACAGGCTAATACCAGAGCATGTGAGGCGACAGATGAATGGTGGCTTTCCA 1265
                                                                                                                                                                                                                                                                                                                  1195 CTAATCAACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCACAGGATTACAA 1251
                                                                                            1015 GCAATAGACCTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACTGCGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="RAFL4"
/note="Site 1: SstI; Site 2: XhoI; subjected
cold-treated(1,2,5,10,24 hr)"
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larity 99.7%; Pred. No. 9.8e-132;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
|mol_trype="mRNA"
|db xref="taxon:3702"
|clone="RAPL04-19-E04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="rosette plants"
/lab_host="SOLR"
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1. .709
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AV782577.1 GI:19801367
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                                                                                                                    Gaps
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                                                                                  Length 1461
                                                                            58.0%; Score 949.4; DB 3; Length 85.8%; Pred. No. 4.7e-181; ive 0; Mismatches 171; Indels
    1. .1461
/gene="At1g06390"
                                                                                              Best Local Similarity 85.8 Matches 1079; Conservative
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Oryza sativa (indica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
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Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
Manalysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
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Email: chenchen@genomics.org.cn
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Tel: 86-10-80481559
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
Location/Qualifiers
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1 (bases 1 to 1745)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Arthur, L.W., Hanafey, M., Consensus Sequences for Design of Overgo Probes
Unpublished (2002)

2 (bases 1 to 1745)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /notes this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project."
                                 CGGTCTTCTCCAATATTCACCAAGTCTACGCTGCACTGCTCTTGACGCATGTGCACATTC
                                                                                                  CTTCTTGATGAGCTACGAGAGCCCAATGCAGCCTGCCAAATGGTCGTCCATTCCCTCC
                                                                                 GTTTTCAATGAACTCCGTGAGCCAAATGCTCGTCTTCCAAATGGCCGACCTCTACCACC
                                                                                                                                                GTTGTTCAACTTCAAACAAGAGTTGTCTGGGGCTTCACCGGAGCTTATCAACAGGCTAAT
                                                                                                                                                                   1083 TCTGTTCAACTTCAAGCATGAACTAGCCAGGGCCTCTCCAGAACTCATCCACAGGCTCAT
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/clone_lib="Maize Mapping Project/DuPont Cornsensus
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.larity 75.3%; Pred. No. 1.6e-127;
Conservative 0; Mismatches 280; Indels
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/db_xref="MaizeDB:634287"
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26a mays PC0077512 mRNA sequence.
AY106255
AY106255.1 GI:21209333
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DEFINITION
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AUTHORS
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Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
31-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9660
Fax: 81-298-36-960
Fax: 81-298-360
Fax: 81-298-36
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Arabidopsis thaliana

Bukaryota, Viridiplantae, Etreptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatorphyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 690)

Seki, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishil, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
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                                                                                                                                                                                                                                                                                                                                                                  541 AAAATGCCGCCTTATGGAATGAAGGAGGAGGATTTACTTCTCTCTGATTAACTAAGTA 600
                                                                                                                                                                              GGTGGCTTTCCATTTCAGCTGGACCCTAGAAAAGCGATCTCGAGATGCTTTTCCAGAGC
GCTCGTCTTCCAAATGGCCGACCTCTACCACCGTTGTTCAACTTCAAACAAGAGTTGTCT
                                                                                             GGTGGCTTTCCATTTCAAGCTGACCCTAGAAAAGCGATCTCGAGATGCTTTTCCAGAGC
                                                                                                                                                                                                                                                                                                        AAAATGCCGCCTTATGGAATGAAGGAGAGGGAGTTTACTTCTCTCTGATTAACTAAGTA
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/note="Site 1: Sat1; Site 2: XhoI; subjected to
dehydration-treated(1,2,5,10,24 hr)"
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/lab_host="SOLR"
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/db_xref="taxon:3702"
/clone="RAFL05-02-L16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1434 AATCAGGAGGCGATGATTGTGTCC 1457
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                             BPS60588 RAFL4 Arabidopsis thaliana cDNA clone RAFL04-12-J20 5',
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Nakajima,M., Enju,A., Akiyama,K., Oono,Y., Muramatsu,M.,
Nayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
Punctional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
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                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for further details.
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/note="Site 1: SstI; Site 2: XhoI; subjected
cold-treated(1,2,5,10,24 hr)"
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41.6%; Score 680.4; DB 5;
Best Local Similarity 99.6%; Pred. No. 8.1e-127;
Matches 681; Conservative 0; Mismatches 3;
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/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL04-12-J20"
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/lab_host="SOLR"
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JOURNAL
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-96-96
Email: meski@rtc.riken.go.jp
Please viait our web site (http://pfgweb.gsc.riken.go.jp/)
further details:
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                                                                                                                                                                                                                                                              /clone lib="RAFL4"
/note="Site 1: Sst1; Site 2: XhoI; subjected
cold-treated(1,2,5,10,24 hr)"
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                                                                                                                                                   thaliana'
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/organism="Arabidopsis thalia/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL04-19-B04"
/dev_stage="rosette plants"
/lab_host="SOLR"
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 683)
Seki,M., Narusaka,M., Rkmiya,A., Ishida,J., Satou,M., Sakurai,T.,
Nakajima,M., Enju,A., Akryama, K., Oono,Y., Muramateu,M.,
Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
Parakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
Punctional annoctation of a full-length Arabidopsis cDNA collection
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                                                                                                                                CACCCTTGGCATAAGGTTTTCCACAAGCGGATGCCTCCGGAAGCCATTGACCTTGCATCT
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Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
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Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tbgr.org; or NCBI, www.ncbi.nlm.ih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, lowa State, then clones may be requested from ZmDB:
                             HTC 16-OCT-2002
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                                                                                                                                                                                                                                  Embryophyta; Tracheophyta;
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Unpublished (2002)
2 (bases 1 to 1666)
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                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                          RESULT 11
CK266410
LOCUS
                                                                                                                                                     ACCESSION
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                                         FIKEN GENOMIC SCIENCES CENTER
3-1-1 Koyada, Taukuba, Ibaraki 305-0074, Japan
7-1-1 Koyada, Taukuba, Ibaraki 305-0074, Japan
7-1-1 81-298-36-9060
Fax: 81-298-36-9060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="RAFLS"
/note="Site_1: SatI; Site_2: XhoI; subjected to
dehydration-treated(1,2,5,10,24 hr)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.9%; Score 620; DB 1; Length 658;
99.7%; Pred. No. 1.2e-114;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                 organism="Arabidopsis thaliana"
Contact: Motoaki Seki
Plant Functional Genomics Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RAFL05-02-L16"
/dev stage="rosette plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATATNCATACTGCTCCTGGTGT 658
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Best Local Similarity 99.7
Matches 620; Conservative
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/done lib="potato ablotic stress cDNA library"
//lone lib="potato ablotic stress cDNA library"
//note="Vector: DCNVSport6.1; Site_1: EcoR1; Site_2: Not1;
supplier: Solamum tubercoum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Ablotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed coots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
CK266410 924 bp mRNA linear EST 03-AUG-2004 EST712488 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAC457 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="abiotic stress treated leaf and root tissue"
/lab host="DH10B-TonA"
                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; Jamiids; Solanales; Solanaceae; Solanum.

1 (bass) Lamiids; Solanales; Solanaceae; Solanum.

1 (bass) Lo 924)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

Generation of ESTs from abiotic stressed potato tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/ . Seg primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGTCCTTTGGGATAGTGTTTCAGGCAAAATGCTTGGAAACTGGAGAGACTGTGGCCATAA
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/organism="Solanum tuberosum"
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAC457"
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                                                                                                                                                                  CK266410.1 GI:39823388
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Contact: Robin Buell
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Best Local Similarity 79.3
Matches 729; Conservative
                                                                                                                                                                                                                                                                                            Solanum tuberosum
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Muitch Information center for Protein Sequences). S prime and 3 prime are assembled with Phrap.
mmple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
nole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
Combined Approach to Evaluate and Improve Arabidopsis Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

Location/Qualifiers

Location/Qualifiers

1. 1638

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llarity 72.3%; Pred. No. 5.1e-111;
Conservative 0; Mismatches 303;
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Matches 797,
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
                                                                                                       TCTTCCTCAATCTCGTTATGGAGTATGTACCAGAGACATTGTACCGGGTT
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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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/db_xref="MaizeDB:638897"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
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    State, then clones
                                                                              organism="Zea mays"
                                      Location/Qualifiers
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    Schnable, Iowa
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
If you are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
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                      ATCGTGACATAAAAACCTCAAAAACTTGTTGGTAAATCCGCACACTCATCAAGTAAAGCTAT
                                                                                                CGAGGTATTACAGAGCACCTGAACTCATCTTTGGAGCAACCGAGTATACGACACACATTG
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Hainey, C.F., Dolan, W., Miao, C.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanefey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design overgo Probes
Unpublished (2002)
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RESULT 14 AV829186 LOCUS DEFINITION

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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2295 bp DNA linear GSS 21-SEP-2004 OSIFCC011089 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence. CL964803.1 GI:52384296
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryzae; Oryza.

1 (bases 1 to 2255)
Ma, L., Wango, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Yiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., An and Wang, J. Sun, D., Lanscriptional regulation of the rice genome and ints comparison to Arabidopsis
Unpublished (2004)
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300,
Tel: 86-10-80481559
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Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and Xhol was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
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MRV82186 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-40-M14 5',
mRNA sequence.
AV829186
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                                              ACCCTTGGCATAAGGTTTTCCACAAGCGGATGCCTCCGGAAGCCATTGACCTTGCATCTC 1047
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Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shibatawa, A., Muzamatau, M., Hayashizaki, Y. and Shinozaki, K.
                       987
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-439
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/clone="RAFL09-40-M14"
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/note="Site 1: BamHI;
dehydration (1, 2, 5,
hr) treatments"
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CCCTTGGCATAAGGTTTTCCACAAGCGGATGCCTCCGGAAGCCATTGACCTTGCATCTCG 1048
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1. .2295
/organism="Oryza sativa (indica cultivar-group)
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="denomic BAP"
/clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequen
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                                                                                                                                 Length 2295;
                                                                                                                                 Query Match 35.4%; Score 578.8; DB 9; Length Best Local Similarity 75.6%; Pred. No. 2.7e-106; Matches 718; Conservative 0; Mismatches 232; Indels
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                                                      1 (Dases 1 to 1670)
Shim, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J.,
Bowser, L., Carainci, P., Chang, E., Dale, J.M., Goldsmith, A.D.,
Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M.,
Nguyen, M., Ondofara, C.S., Palm, C.J., Quach, H.L., Sakurai, T.,
Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,
Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
Theologis, A. and Ecker, J.R.
Arabidopsis cDNA clones
Unpublished
I. Chang, M., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D.,
Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M.,
Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T.,
Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,
Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
Theologis, A. and Ecker, J.R.
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TTSKDELFLALVMEYVPESLYRVLKHYSSANOPMPLVYVKLYMYQIFRGLAYIHNVAG
VCHRDLKPQNLLVDPLTHQVLFCFGSAKQLVKGEANISYICSRFYRAPELIFGATEY
TTSIDIWSAGCVLAAELLLGOPLFPGENAVDGLWEIKTGFPTREERRCWNHYTDFR
FPQIKAHPWHKIFHKRMPPEAIDFASRLLQYSPSLRCTALEACAHPFFDEHREPNARL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-JAN-2002) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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      Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheo
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/organism="Arabidopsis thaliana"
/moll type="mRNA"
/db_xref="taxon:3702"
/chromosome="4"
/clone="RAFL02-10-D23(R21695)"
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/product="AT4918710/F28A21_120"
/protein_id="RAL/7705.1"
/db_xref="GI:18700188"
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/replace="a"
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Score 1596.4;

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Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length CDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Lake ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequences from Col-0. full-length clones. Ceres, Inc. carried out the clustering of the full-length clones. Ceres, Inc. carried out the clustering of the closes, selection of clones, and sequence assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /traislation="MiddKeWpaavvDGHDQvTGHIISTTIGGKNGEPKQTISYMAER
VQCGSGFQTVPQAKCLETGETVAIKVCTQDRRYKNRELQLWRWMDHPWVCCLKGFFS
TTSKDELFLAILWEYVPESLYRVLKHYSSANQRMPLVYVKLYMYQIFRGLAYTHNVAG
VCHRDLKFQNLLVDPLTHQVKICDFGSAKQLVKGEANISYICSRFYRAPELIFGATEY
TTSIDIWAGACCVLAELLLQQPLFFGERANDVQDLWBIIKVCTRFYRERIRCMNPHYTDFR
FPQIKAHPHKIEFKRMPPRAIDFSRLLQVSPSLACTALBACAHPFDELREPNARL
PNGRPPPPLNFKQEVAGSSPELVNKLIPDHIKRQLGLSFLNQSGT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="shaggy-like protein kinase etha (EC 2.7.1.-)"
/protein_id="AAM63594.1"
/db_xref="GI:215254512"
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/db_xref="taxon:3702"
/clone="256076"
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         Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N.,
Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
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Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
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Brover,V. Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R.
Feldmann,K.
Full'Length cDNA from Arabidopsis thaliana
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Arabidopsis thaliana clone 256076 mRNA, complete sequence.
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Identification of novel e2f target genes 
Patent: WO 2004035798-A 1279 29-APR-2004;
CropDesign N.V. (BE)

    1143
    ^organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

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from Patent WO2004035798
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Sequence 1279 from Pate:
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SENDAVTGHITSTTIGGKWOBERQTI SYMARKYGTGSFGIPUPQAKCLEGGESVAIKK
VLQDRRYKRRELQLAGGERGAT SYMARLMDHPNVVSLKHCFSTTADBLFLNLVMEYVPETLYRVLKH
YTSSNQRMPIPVKLYTYQIPRGLAYIHTAPGVCHRDIKPQNLLVDPHTHQCKLCDFG
SKVLVKGEPRISYICSRYRAPBLIFGGTBYTSSIDIWAGGVLABLLLGQPLFPGE
NSVDQLVBIIKVLGTPREEIRCAMNNYTDFRPPQIKAHPWHKVFHKRMPPRAIDLAS
RLLQYSPSLRCTALEACAHPFVBELREPNARLDNGRPLPPEPFFFRFRENCE
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Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud,
Institut de Biotechnologie des Plantes, Centre de Recherches sur
les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405
ORSAY Cedex, PRANCE
Corresponding genomic sequence: Y09300.
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/db_xref="UniProt/Swiss-Prot:Q39010"
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A.thaliana mRNA for shaggy-like kinase dzeta.
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protein_id="CAA64408.1"
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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Columbia ecotype"
/db_xref="taxon:3702"
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1036 1096 1156 1216 1276 977 AATCAAAGCCCACCCTTGGCATAAGGTTTTCCACAAGCGGATGCCTCCGGAAGCCATTGA 1036 1037 CCTTGCATCTCGGCTTCTTCAATACTCACCAAGTCTACGTTGCACTCGCGCTCGAGGCATG 1096 1156 1157 TCTACCACCGTTGTTCAACTTCAAACAAGAGTTGTCTGGGGCTTCACCGGAGCTTATCAA 1216 376 436 376 496 556 919 796 736 856 916 916 916 256 436 556 496 919 919 736 919 796 856 857 GITATICCCGGGAGAAATICTGTGGACCAGCTAGTGGAGATCATAAAGGTTCTTGGTAC 916 Tracaresceracererrerresaacacarearerrescaarrerarrecaescaaaare 317 CTTGGAAACTGGAGAATCAGTAGCCATTAAGAAGGTTTTGCAAGATCGCCGTTATAAAAA 737 AGTCAAAATCTGTGACTTTGGCAGTGCGAAACAGCTCGTTAAAGGTGAACCAATTTC TTACATCTGCTCACGATTCTACCGTGCACCCGAGCTCATATTTGGTGCCACTGAGTACAC AACTICIATICA TAICTGGICTGCTIGGTIGTGTTCTTGCTGAGCTICTTCTTGGTCAGCC. 197 CGGTCACATAATTTTCTACTACAATTGGAGGCAAAAATGGTGAACCTAAACAGACCATTAG 497 AGAGACATTGTACCGGGTTTTGAAGCACTATACTAGTTCAAACCAGCGGATGCCTATCTT GTGTAAGCTCTGTGATTTTGGAAGTGCAAAAGTACTGGTGAAAGGTGAACCAAACATATC 1097 IGCGCATCCGTTTTTCAATGAACTCCGTGAGCCAAATGCTCGTCTTCCAAATGGCCGACC craricroaacriracacaraccaaarcricagaggcriggcrirararccaracrgcrcc 617 TGGTGTCTGCCACAGAGATATAAAACCACAAAATCTTTTGGTTGATCCCACACCCATCA ATCATCCATTGATATATGGTCTGCTGGTTGTGTTCTGGCAGAGCTACTTCTTGGGCAGCC 917 recaacrescaasaaarecesresareaaaceaaacracasaacrescaca 1097 TTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCACAGCGCTCGAAGCTTG TCTCCCCCCTCTCTTCAACTTCAAACAAGAAGTAGCTGGATCATCACCTGAACTGGTCAA caescraaraccasascarersassessas careares respectras carricas secres TITGGAGACTGGAGAAACCGTGGCGATAAAGAAGGTTTTGCAAGATAGAAGATACAAGAA 437 TTTCTTCTTCTACAACGACTAGAGATGAGCTCTTCCTCAATCTCGTTATGGAGTATGTACC GGGAGTTTGTCACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCTCTTACTCATCA 917 ATTATTCCCCGGAGAAATGCTGTGGATCAGCTCGTGGAAATTATAAAGTTCTTGGTAC 977 ACCAACTCGAGAAGAATCCGTTGTATGAATCCCAACTACACAGATTTCAAGTTCCCACA GATAAAGGCCCATCCCTGGCACAAGATCTTCCACAAAAGGATGCCCCCAGAAGCGGTTGA TGCACATCCGTTCTTTGATGAACTCAGAGAACCAAACGCTCGTTTACCAAATGGACGGCC CTTCTTTTCGACTACAGAGAAGACGAGCTTTTCTTGAACTTGGTTATGGAGTATGTCCC CTATGTTAAACTTTACAGTTATCAGATCTTCCGGGGACTTGCTTACATTCACAGTTGCCC 1277

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CGCCATGGCTGATAAAGAGATGCCTGCTGCTGTTGATGGACATGATCAAGTCAC

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/trainiation="Wisiplopppesladopphilhggdslkrrpdidndkemsaavi
Erdnangelistigemerrorskolskydskydisterestynikk
VLQDRXYKRELQLMRLMDHPNVSLKHCFPSTTTRDELFLNLVMSYVPETLYRVLKY
YTSSNQRMPIFYVLTYQIFRGLATHTAPACVCHRDYKPQNLLVDPLTHQCKLCVFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 CTIGGAAACTGGAGAATCAGTAGCCATTAAGAAGGTTTTGCAAGATCGCCGTTATAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 TTTGGAGACTGGAGAACCGTGGCGATAAAGAAGGTTTTGCAAGATAGAAGATACAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            857 AACTICIATIGATATCIGGICIGCIGGITGITCITGCIGAGCITCITCITGGICAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 TGGTCATATTATTTCCACCACAATCGGTGGCAAAATGGTGAACCAAAACAGACAATTAG
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                                                                                                                                                   /product="putative shaggy protein kinase dzeta"
/protein_id="AAM20332.1"
/db_xref="GI:20465727"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 733; DB 8;
Pred. No. 6.1e-177;
                                                                                                                      /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="At2g30980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.4%;
Matches 889; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317
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                                                                                                                                                                                                                                             AY096698 1270 bp mRNA linear PLN 18-SEP-2002
Arabidopsis thaliana putative shaggy protein kinase dzeta
(At2310980) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Labases 1 to 1270)
Yamada, K. Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Mayers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Scki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A., Arabidopsis, Open Reading Frame (ORF) Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, Can 94710, USA
The RIEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA: RIKEN Arabidopsis Full-Length cDNA): Seki,M., Narusaka,M., Ishida,J., Sakushi,Y. and Shinozaki,Y. carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriuni, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J. Shinozaki, K., Davis, R.W., Ecker, J.R., and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORP) clones using the RAFL cDNAs: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E. Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Criumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /ecotype="Columbia"
/note="This clone is in pUNI 51."
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/db_xref="taxon:3702"
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1345
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1337
                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
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Arabidopsis thaliana

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 1566)

Yamada, K., Liu, S. X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,

Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L.,

Carninoi, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,

Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,

Lin, J., Miranda, M., Shinn, P., Southwick, A., Shinozaki, K.,

Davis, R.W., Ecker, J.R. and Theologis, A.,

Arabidopsis Full Length CDNA Clones

L Unpublished
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Submitted (19-NOW-2001) Plant Gene Expression Center, 800 Buchanan
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                                                                                                                                                                                                       933 AATCAAAGCCCACCCTTGGCATAAGGTTTTCCACAAGCGGATGCCTCCGGAAGCCATTGA
                           GTTATTCCCGGGAGAAATTCTGTGGACCAGCTAGTGGAGATCATAAAGGTTCTTGGTAC
                                                                           ACCAACTCGAGAAATCCGTTGTATGAATCCCAACTACACAGATTTCAAGTTCCCACA
                                                                                                               873 TCCAACTCGCGAAGAAATCCGGTGCATGAACCCAAACTACACAGACTTCAGATTCCCACA
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Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
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/translation="MYSIPLGPPQPPSLAPQPPHLHGGDSLKRRPDIDNDKEMSAAVI
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YTSSNQRMPIFYVTYQIFRGLAYIHTAPEVCHRDVKPQNLLVDPLTHQCKLCDFG
SAKVLVKGEANISYICSRYXRAPELIFGATEYISSIDIMSAGCVLAELLLGQPLFPGB
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The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Yamada, K., Banh, J., Bann, F., Dale, J.M., Goldsmith, A.D., Lee, J.M., Conodera, C.S., Quach, H.L., Tang, C.C., Tortumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Chen, R., Jones, T., Karlin, Neumann, G., Kim, C., Kossema, E., Lam, B., Lin, J., Meyers, M.C., Davis, R.W., Ecker, J.R. and Theologis, A., Southwick, A.,
                                                                                                                                                                                                                                                                                                                                                                                                    Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers
1. .1566
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                                                                                                                                                                                                                                                                                 Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
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/note="This clone is in a modified pBluescript vector
(Lambda ZAP) as a XhoI/SatI insert."
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/protein id="AAL16376.1"
/db_xref="GI:17381128"
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/db_xref="taxon:3702"
/chromosome="2"
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/gene="At2g30980"
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Matches 889; Conservative
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and Ecker, J.R.
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                                                                                                                                                                                                                                                                                         626 TGGTGTCTGCCACAGAGATGTGAAACCACAAAATCTTTTGGTTGATCCCCTCACCATCA 685
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                                                                                                                                                                                                                                                                                                                                                                    GTGTAAGCTCTGTGATTTTTGGAAGTGCAAAAGTACTACTGGTGAAAGGTGAAGGCAAACATATC
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                                                                                                                                                                                                                                          677 GGGAGTTTGTCACAGAGATCTAAAAGCCTCAAAAICTTCTGGTTGATCCTCTTACTCATCA
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Arabidopsis thaliana (thale cress)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Arabidopsis thaliana

(bases 1 to 1591)

REFERENCE

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Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, B., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawi, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Mayyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamuray, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Arabidopsis cDNA clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (08-APR-2002) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCCATGGCTGATAAGGAGATGCCTGCTGCTGTAGTTGATGGACATGATCAAGTCAC 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shim, P., Chenk, R., Kim, C.J., Meyers, M.C., Banh, J., Boshin, P., Chen, H., Cheuk, R., Chang, E., Dale, J.M., Goldsmith, A.D., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satu, M., Southwick, A., Tang, C.C., Torlumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
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Pred. No. 6e-177;
0; Mismatches 260; Indels
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                                                                                                                                               PLN 22-OCT-1996
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Arx etha gene; shaggy-like kinase etha.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Virtidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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2519. .2575,2670. .2810,2901. .2951,3032. .3127,3214. .32
3380. .3577)
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Submitted (18-OCT-1996) M.C. Dornelas, Universite de Paris Sud
(Paris XI), Institut de Biotechnologie des Plantes, Lab. Biol. developpement des Plantes, Batl. eFRANCE
                                                                                                                                               linear
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/organism="Arabidopsis thaliana"
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1157. .1745
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Dornelas, M.C.
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  AACTTAAAA 1345
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42.1%; Score 732; DB 8;
Best Local Similarity 69.8%; Pred. No. 1e-176;
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
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                                                           3428 GCTCGTTTACCAAATGGACGGCCTCTCCCGCCTTCTTCAACTTCAAAGAAGTAGCT
                                                                                                  GGATCATCACCTGAACTGGTCAACAAGTTGCAGACCATATCAAGAGACAATTGGGT
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                                                                                                                                                           CTAAGCTTCTTGAATCAATCTGGAACTTAAAAGGGATCCTGCAAAAGACAACTACTTTTT
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Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N. Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome
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Brover,V. Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R.
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Full-Length cDNA from Arabidopsis thaliana
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Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R.
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this set was done by comparison with known proteins: two percent the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ArG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Wa or LiAer ecotypes and therefore may contain polymorphisms when compared to sequences from Col.0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the Location/Qualifiers /translation="WISIPLGPPQPPSLAPQPPHLHGGDSLKRRPDIDNDKEMSAAVI
SENDRYTGHISTTORGAKLETGESVAIKK
VLODRRYKRRELQLATGCKNOSEKQITSYAMERVYGTSFGTIVORAKLETGESVAIKK
VLODRRYKRRELQLATGCKNOSEKAICPFSTTTRDELFLALVMBYVPETLYRVLKH
YTSSNQRMPIFVKLYTYQIPRGLAYIHTAPGVCHRDVKPQNLLVDPLTHQCKLCDFG
SKYLVKGERANISYICSRYKRSPELIFGATEVTSSIDIWAGCYLLAELLLGQPLPGE
NSVDRLVSIIKVLGTPTREIIRCMANPYTDFRFPQTKAHPWHKVFHKRMPPAIDLAS
RLLQYSPSLMCTALAFGAHPFPRELIRCMANPATDNRRPDPLFNFKQELSGASPELINA ö 205 445 256 316 376 616 676 325 436 496 556 505 625 257 TGGTCATATTTTCCACCACACATGGCGAAAATGGTGAACCAAAACAGACAATTAG TTACATGGCGGAGCGAGTTGTTGGTACAGGCTCGTTCGGGATCGTTTTCCAAGCAAAATG 26 TTACATGGCCGAACGTGTTGGAACAGGATCATTCGGAATTGTATTCCAGGCAAAATG 326 crioganaciogaganicaciaccarinagangariringcangarcecerranana 386 ccsacacriccaarraarcccacraarccarccaaarcrecriccarccaraccarric 446 Tricricricracaacgacragagargagcrcriccrcaarcrcgrrarggagrafgracc 557 TGAGACGTTGTATCGAGTTCTGAAACATTATAGTAGTGCAAAACCAAAGAATGCCTCTTGT CTATGTTAAACTTTACAGTTATCAGATCTTCCGGGGACTTGCTTACATTCACAGTTGCCC CGCCATGGCTGATGAGGAGATGCCTGCTGTGGTTGATGGACATGATCAGTCAC TTTGGAGACTGGAGAACCGTGGCGATAAAGAAGGTTTTGCAAGATAGAAGATACAAGAA CTTCTTTTCGACTACAGAGAAGACGAGCTTTTCTTGAACTTGGTTATGGAGTATGTCCC Gaps product="putative shaggy-like protein kinase dzeta"
protein\_id="AAM65084.1"
/db\_xref="G1:21593135" ö 42.0%; Score 729.8; DB 8; Length 1503; llarity 77.2%; Pred. No. 4e-176; Conservative 0; Mismatches 262; Indels 0;

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/t-anslation="WASLPLGPOPHALAPPLQLHDGDALKRRPELDSDKEMSAAVIEG
NDAVTGHIISTTIGGKNGEPKQTISYMAERVVGTGSFGIVFQAKCLETGESVAIKKVL
OBDRRYKNREDLAMRPHDHPNISLAHETFSTTSRDELFULWERVPETLYRVLRHYT
SSNQRMPIFYVKLYTYQIRFGLAYTHTVFGVCHRDVKPQNLLVDPETHQVKLCDFGSA
KVLVKGEPNISYICSRYYRAPELIFGATEYTASIDIWSAGCVLAELLLGQPLFPGENS
VDQLVBIIYUTGTPTREBIRCHNPNYTDFRPPQIKAHPWHKVFHKRNPPBAIDLASRL
DEHVRRQMSTGLQNS
PEHVRRQMSTGLQNS
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Center, Gyeongsang National University, Chinju 660-701,
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Pred. No. 1.7e-169;
0; Mismatches 260; Indels
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                                                                       thaliana"
                                                                                                                                                                                                                                               /product="GSK3/shaggy-like
/protein_id="AAB71545.1"
/db_xref="G1:2444277"
                                                               /organism="Arabidopsis
/mol_type="mRNA"
/strain="Columbia"
                                                                                                                    /db_xref="taxon:3702"
                                      Location/Qualifiers
                                                                                                                                                                                                                                    /codon start=1
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Local Similarity 76.8%;
nes 860; Conservative
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Arabidopsis thaliana GSK3/shaggy-like protein kinase (GSK1) mRNA,
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Arabidopsis thaliana
Brabidopsis thaliana
Brantophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.

1 (bases 1 to 1572)
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1 (bases 1 to 1572)
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Direct Submission
Submitted (18-AUG-1997) Plant Molecular Biology and Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An Arabidopsis GSK3/shaggy-like gene that complements yeast salt
stress-sensitive mutants is induced by NaCl and abscisic acid
Plant Physiol. 119 (4), 1527-1534 (1999)
                                                            GTGTAAGCTCTGTGATTTTTGGAAGTGCAAAAGTACTGGTGAAAGGTGAAAGCAAACATATC
                                                                                                                                 ATATATCTGCTCTCGGTATTACCGATCTCCAGAACTCATCTTTGGTGCCACAGAGTATAC
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   TGGTGTCTGCCACAGAGATGTGAAAACCACAAAATCTTTTGGTTGATCCCCTCACCATCA
                                      AGTCAAAATCTGTGACTTTGGCAGTGCGAAACAGCTCGTTAAAAGGTGAACCAAACATTTC
                                                                                                           TTACATCTGCTCACGATTCTACCGTGCACCCGAGCTCATATTTGGTGCCACTGAGTACAC
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Plao,H.L., Jang,H.J., Pih,K.T., Lim,J.H., Kang,S.G., Jin,J.B.
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99596) (PGR97-008) Plant Physiol. 113, 306-306 (1997) 2 (bases 1 to 1614)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (01-AUG-1996) M.C. Dornelas, Universite De Paris-Sud
(Parisxi), Institut De Biotechnologie Des Plantes, Lab. Biol. Du
Developpement Des Plantes, Batiment 630, F-91405 Orsay Cedex,
                                                                                                                                                                 CTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTAGGTTCCCACAAATCA
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 TCTGCTCCCGTTATTATCGTGCTCCAGAACTCATCTTTGGCGCCCACAGAGTATACAGCAT
                                            CCATAGATATATGGTCTGCTGGTTGTACTGGCAGAGCTTCTTCTTGGCCAGCCGTTAT
                                                                                                    TTCCAGGAGAAAATTCAGTTGATCAGCTTGTGGAGATCATAAAAGGTTCTTGGTACTCCAA
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                                                                                                                                                                                                                                                                                                                                                                            CGCCTCTCTTCAACTTCAAACAAGAAGTAGCTGGATCATCACCTGAACTGGTCAACAAGT
                            CTATTGATATCTGGTCTGCTGGTTGTTTTGCTGAGCTTCTTCTTGGTCAGCCATTAT
                                                                                     TCCCCGGAGAAAATGCTGTGGATCAGCTCGTGGAAATTATTAAAGTTCTTGGTACACCAA
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/tissue type="roots"
/clone_lib="lambda ZAPII"
/dev_stage="young shoots"
/note="ecotype Columbia"
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1. .1614
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73. .1296
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Pred. No. 1.7e-169;
0; Mismatches 260; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 40.5%; al Similarity 76.8%; 860; Conservative
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Best Local Si
Matches 860;
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622 TTAAACTTTACAGTTATCAGATCTTCCGGGGACTTGCTTACATTCACAGTTGCCCGGGAG 681
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product="putative shaggy kinase"
/protein_id="AAK93730_1"
/db_xref="G1:15293239"
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                                                                                                                                                                                               1. .1255
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                         ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="At1g06390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="At1g06390"
                                                                                                                                                                                                                                                                                                            chromosome="1"
                                                                                                                                                                                                                                                                                                                                              /clone="U09338"
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Arabidopsis thaliana putative shaggy kinase (At1g06390) mRNA,
complete cds.
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1 (bases 1 to 1255)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,P., Kaelin-Neumann,G., Kin,C., Lam,B., Miranda,M., Nguyen,M., Palm,C., Lam,B., Miranda,M., Nguyen,M., Palm,C., Lam,B., Miranda,M., Nguyen,M., Palm,C., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and
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The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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Direct Submission
Submitted (02-AUG-2001) Plant Gene Expression Center, 800 Buchanan
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                                                                               1042 AGGCCCATCCCTGGCACAAGATCTTCCACAAAAGGATGCCCCCAGAAGCGGTTGATTTGG
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COMMENT

ö 261 151 211 271 441 331 501 391 561 451 621 Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers 262 ATATTATTTCCACCACACTCGGTGGCAAAATGGTGAACCAAAACAGACAATTAGTTACA 321 322 TGGCGGAGCGAGTTGTTGGTACAGGCTCGTTCGGGATCGTTTTCCAAGCAAATGTTTGG 381 Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs. 272 AAACTGGAGAATCAGTAGCCATTAAAAGGTCTTGCAAGATGGACGCTATAAAAACGTG 332 AGTIGCAACTAATGCGACCAATGGATCACCCAAATGTCATCTCCTTGAAGCACTGTTCT 562 CGTTGTATCGAGTTCTGAAACATTATAGTAGTGCAAACCAAAGAATGCCTCTTGTCTATG 202 TGGCTGATGATAAGGAGATGCCTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGGTC 92 regarrerdaraaccaariererecaeererrarreaeccaaareaeererraereere 382 AGACTGGAGAAACCGTGGCGATAAAGAAGGTTTTGCAAGATAGAAGATACAAGAACCGAG 442 AACTICAGTIGATGCGTGTGATGGATCATCCGAATGTGGTTTGTTTGAAGCATTGCTTCT TITCGACTACAGAGAAGACGAGCTITICITGAACTIGGTTATGGAGTATGTCCCTGAGA 'note="contains an eukaryotic protein kinase PF | 00069 Gaps ; 0 Length 1255; Indels

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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 1582)

I (bases I to 1582)

I (bases I to 1582)

Yamada, K., Liu, S. X., Sakano, H., Pham, P. K., Banh, J., Chung, M. K., Goldsmith, A.D., Lee, J. M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninoi, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nauyen, M., Palm, C., Lam, B., Lin, J., Miranda, M., Saki, M., Saki, M., Saki, M., Saki, M., Saki, M., Shinn, P., Southwick, A., Shinozaki, K., Arabidopsis Pull Length CDNA Clones

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Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G.,
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KUYKGEPPU SYLCSRYYRAPBLI FGATBTYASID WSAGGVLAELLIGOPL PRGENS
VDQLVEI IKVLGTPFREEI RCMNDPYTDFR FPQI KAHPWHKVFHKRMPEA IDLASRI
LQYSPSLRCTALBACAHPFPNELREDNARLPNGRPLPPLFNPKQELGGASMELINRLI
                                                                                                                                                                                                                          Direct Submission
Submitted (03-MAY-2001) Plant Gene Expression Center, 800 Buchanan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing and annotation of the RAFL CDNAs: Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jonest, Xarlin-Neumann,G., Kim,C., Koesema,E. Lam,B., Lih,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Annotation is based on the January 2002 version of the Arabidopsis
Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                Street, Albany, CA 9471, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="This clone is in a modified pBluescript vector
(FLC-1) as a BamHI/XhoI insert."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Salk, Stanford, PGEC (SSP) Consortium members carried out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1582;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome submitted to GenBank.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ecotype="Columbia"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss. Arabidopsis thaliana DNA fragment SEQ ID NO: 52951. AAC47206 standard; DNA; 1745 BP. 99US-0121825P. 99US-0123180P. 99US-01257848P. 99US-0126264P. 99US-0126785P. 99US-0126785P. 99US-0128234P. 99US-0128745P. 99US-0130449P. 99US-0130449P. 99US-0130449P. 99US-0132048P. 99US-0132407P. 99US-0132484P. 25-FEB-2000; 2000EP-00301439 9US-0132485P (first entry) Arabidopsis thaliana EP1033405-A2. 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 18-OCT-2000 06-SEP-2000 25-FEB-1999 30-APR-1999 29-MAR-1999 01-APR-1999 06-APR-1999 19-APR-1999 28-APR-1999 08-APR-1999 21-APR-1999 AAC47206; RESULT 1 AAC47206 

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666	Oy 869 TATCTGGTGGTTGTTGTTGTTGTTGTTGTTGTTGGTGGTCGTC
; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	. Qy 929 AGAAAATGCTGTGGATCAGCTCGTGGAAATTATTAAAGTTCTTGGTACACCAACTCGAGA 988
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                 1440 ACAPAGCCAGCTGCTAGCAAAACCAACTACCCAAATCTGCGAAAAACAAAAAACTCTCCAGT 1499
                                                      Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana DNA fragment SEQ ID NO: 55886.
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Query Best Match	تر ده زو	3; Length 1657; 7; Indels 3; Gaps 3;
<i>&amp;</i>	138 CTCTCTCTCAAATCCACTCT-CTCTTTTTTTTTTTTTTT	CTCTTCTCCTCTGTGTCTCTAT 196
QQ	TCTCTCAAATCCACTCTGCTCTTTTTTTTTTTTTTTTTT	CTTCTCCTCTGTGTCTCTA
ර සි	197 CGCCATGGCTGATGATAAGGAGATGCCTGCTGCTGTTGATTGA	STTGATGGACATGATCAAGTCAC 256
ò	CATATTACTACCACACAATCG	GGTGAACCAAAACAGACAATTAG 316
qq	136 TGGTCATATTTTCCACCACAATCGGTGGCAAAAA	19
& 8	317 TTACATGGCGGAGCGAGTTGTTGGTACAGGCTCGTTC	CGGGATCGTTTTCCAAGCAAAATG 376
ò	77 TTTGGAGA	CAAGAA 430
qq	256 TTTGGAGACTGGAGAAACCGTGGCGATAAAGAAGGTTTTGCAAGATGAAGAA	
ò	437 CCGAGAACTTCAGTTGAGTGGATGGATGATCCGAATGTGGTTGTTTTTTTT	GAAGCATTG 49
අු	316 CCGAGAACTTCAGTTGATGCGTGTGATGGATCATCC	GAAGCATTG 37
පි සි	497 CTTCTTTTCGACTACAGAGAAAGACGAGCTTTTCTTC	CTTGAACTTGGTTATGGAGTATGTCCC 556
8 8	57 TGAGACGTTGTATCGAGTTCTGAAACATTATAG	CAAACCAAAGAATGCCTCTTGT 61
qq	) m	CAAACCAAAGAATGCCTCTTGT
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qq	496 CTATGTTAAACTTTACATGTATCAGATCTTCCGGGGAC	TTGCTTACATTCACAA
ò	677 GGGAGTITGTCACAGAGATCTAAAGCCTCAAAATCTT	
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QQ	616 AGTCAAAATCTGTGACTTTGGCAGTGCGAAACAGCT	saagccaacatric 679
ò	97 TTACATCTGCTCACGATTCTACCGTGCACCCGAGCT	GCCACTGAGTACAC
g	76 TTACATCTGCTCACGATTCTACCGTGCACCCGAGCT	rat tregreccacreagracae 73
à í	in a	TGAGCTTCTTGGTCAGCC 9
g	36 AACTTCTATTGATATCTGGTCTGCTGGTTGTGT	GETCAGCC 79
à ·	17 ATTATTCCCCGGAGAAATGCTGTGGATCAGCT	7
g	6 ATTATTTCCCGGAGAAATGCTGTGGATCAGCT	CTTGGTAC 855
ራ ብ	977 ACCAACTCGAGAAGAATCCGTTGTATGAATCCCAACTACACAGATTTCAAG	racacagatttcaagttcccaca 1036 
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ò	1097 ITTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCT	CAAGTCTAAGATGCACAGCGCTCGAAGCTTG 1156
οg	CATCAAGGCTCCTTCAATACTCTC	-ย

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The invention relates to an isolated DWARF12 (DWF12) mutant polypeptide.

The mutant polypeptide comprises at least 70 % sequence identity to the amino acid sequence of the DWF12 polypeptide given in the specification at positions 38-326 or 1-380, and having a mutation of at least one noncegon of the polypeptide corresponding to a region given in the specification. The mutant DWF12 polypeptide is useful in producing transgenic plants that display at least one altered blochemistry, structure or morphology. The transgenic plant can be used in plant breeding or incectly in agricultural production or industrial applications. The polymucleotide is useful in isolating or creating other mutant call gene alleles, in inhibiting or enhancing endogenous DWF12 gene expression, and in standard diagnostic assays as hybridisation probe or primer. This polymucleotide sequence represents the cDNA of the wild-type DWF12 locus of the invention
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                                     New isolated DWARF12 mutant polypeptide for producing transgenic plants displaying altered biochemistry, structure or morphology which are useful in plant breeding, in agricultural production or industrial applications.
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                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 1490;
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                                                                                            Example 2; Fig 2; 62pp; English
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Best Local Similarity 98.0%;
Matches 1460; Conservative (
          P-PSDB; AA026726, AA026727.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTCCCGCCTCTTTTCAACTTCAAAGAAGTAGCTGGATCATCACCTGAACTGGTCAA
                                                                                                                                                                                                                                    AGCCACAAAGGTCGTAGTTGAAGGCAAGCGTGGAGGACACAAATTCGAAAGTTTTTCCTCCT
                                                                                                                                                                                                                                                                          CAAACTCGTTCAGACAAAGCCAGCTGCTAGCAAAACCAAACT-ACCCAAATCTGCGAAAAC
                                                                                                                                                                                                                                                                                            CAAACTCGTTCAGACAAAGCCAGCTGCTAGCAAAACCAAACTCCCCCCAAATCTGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                AAAAACTCTCCAGTGTTGTATCTGCTTATTTCTCTTTTCAAGTTTGGTGAAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                               ACAGTCTCCTCTTTCTTTCTTTCTTTCCCCCTTATGTAATGAGTTTAGTCA
                                                                                                         AGCCACAAGGTCGTAGTTGAAGGCAAACGTGGAGGACAACAATTC-AAAGTTTTTCCTCCT
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74tags a
/product= "Protein of wild-type DW12 locus"
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell branacteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thalians atress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                         Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                  Claim 144; SEQ ID NO 875; 577pp + Sequence Listing; English
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                                                                                                                                         (SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                 24-AUG-2000; 2000US-0227866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                        24-AUG-2001; 2001WO-US026685
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Query Match 63.3%; Score 1099.8; DB 6; Length 1143; Best Local Similarity 97.6%; Pred. No. 3.4e-296; Matches 1116; Conservative 0; Mismatches 27; Indels 0;
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Arabidopsis thaliana stress regulated gene SEQ ID NO 875 Arabidopsis thaliana; plant; gene; stress; transgenic;

21-JAN-2003

ABZ13070

Arabidopsis thaliana

BP

ABZ13070 standard; DNA; 1143

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Sequence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;

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Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1279.
                                                                                           gene; ss; plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                                        (first entry)
                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                      WO2004035798-A2
                                                        15-JUL-2004
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20-OCT-2003; 2003WO-EP011658 18-OCT-2002; 2002EP-00079408

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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up characteristics. Specifically, it refers to identifying genes that are up conveniently of a conversegulated in transgenic plants everypeasing the heterodimeric step plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal confiction, storage lipid mobilisation and/or altered photosynthesis, cach relative to the corresponding wild type plants. Accordingly, these each relative to the corresponding wild type plants. Accordingly, these carbon also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polymuclectide sequence is thale cress cDNA curenciption factor, given in an exemplification of the invention.
                                                                                                                                                                             Altering plant characteristics, useful for producing plants for enzyme c
pharmaceutical production comprises modifying in a plant, expression of
one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1279; 134pp; English
                                                 Vlieghe K;
                                                 De Veylder L,
(CROP-) CROPDESIGN NV
                                                                                                  WPI; 2004-348466/32.
P-PSDB; ADN73385.
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560 360 620 420 680 480 260 320 120 380 180 440 240 500 300 9 261 CATATTATTTCCACCACAATCGGTGGCAAAATGGTGAACCAAAACAGACAATTAGTTAC ATGGCGGAGCGAGTTGTTGGTACAGGCTCGTTCGGGATCGTTTTCCAAGCAAATGTTTG GAGACTGGAGAAACCGTGGCGATAAAGAAGGTTTTGCAAGATAGAAGAACCGA GAACTICAGTICATGCGTGTGATGCATCCGAATGTGGTTTGTTGAAGCATTGCTTC TITICGACTACAGAGAAGACGAGCTITICTICGAACTIGGITATGGAGTATGTCCCTGAG ACGITGIATCGAGTICTGAAACATTATAGTAGTGCAAACCAAAGAATGCCTCTTGTCTAT GTTAAACTTTACAGTTATCAGATCTTCCGGGGACTTGCTTACATTCACAGTTGCCCGGGA 1 ATGGCTGATGATAAGGAGATGCCTGCTGTTGATGATGATGATGATGATGATCAAGTCACTGGT 201 ATGGCTGATGATAAGGAGATGCCTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGGT 12; Length 1143; ö Indels Pred. No. 3.4e-296; 0; Mismatches 27; DB Score 1099.8; Query Match 63.3%; Best Local Similarity 97.6%; Matches 1116; Conservative 321 561 381 501 361 621 441 엄 g 요 Š g Š 셤 8 셤 ò 셤 ò ð ઠ ð

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The present sequence is a full-length cDNA encoding BnPK-2, a novel canola protein kinase stress-related polypeptide (PKSRP). The CDNA was identified on the baais of homology to Physcomitralla patens PK-3 (see ACC57962) and PK-10 (see ACC57966) sequence. BnPK-2 is an example of PKSRPs of the invention that are important for modulating a plant's response to environmental stress. Over-expression of PKSRP coding nucleic acids in a plant results in the plant's increased tolerance to environmental stress. Transgenic monocot and dicot plants are provided that show increased tolerance to high salinity, drought and low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 ATAAGTTACATGGCGGAGCGAGTTGTCGGTACAGGCTCCTTCGGGATAGTGTTCCAGGCG 305
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                                                                                                                                                                                          New protein kinase stress-related polypeptide coding nucleic acid, us for producing transgenic plants with an increased tolerance to an environmental stress, e.g. high salinity, as compared to a wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.9%; Score 1058.4; DB 8; Length 1621; Best Local Similarity 81.5%; Pred. No. 1.5e-284; Matches 1307; Conservative 0; Mismatches 271; Indels 26;
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                                         09-NOV-2001; 2001US-0346096P.
       12-NOV-2002; 2002WO-US036374.
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RESULT 8 AAC47571

Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss. Arabidopsis thaliana DNA fragment SEQ ID NO: 54312 9905-0132487P 9905-0132487P 9905-0134218P 9905-0134219P 9905-013421P 9905-013421P 9905-0134941P 9905-0134941P 9905-0134941P 9905-013553P 9905-013553P 9905-013552P 9905-013552P 9905-013552P 9905-013552P 9905-013752B 9905-0139452P 9905-0139452P 9905-0139453P 9905-0139452P 9905-0139452P 9905-0139452P 9905-0139452P 9905-0139452P 9905-0139455P 990S-0128234P. 990S-0128714P. 990S-0129845P. 990S-0130077P. 99US-0132484P. 99US-0132484P. 99US-0132485P. 99US-0132486P. 99US-0130891P. 99US-0131449P. 99US-0132048P. 99US-0121825P. 99US-0123180P. 99US-0123548P. 99US-0125788P. 99US-0126785P. 99US-0130510P (first entry) 99US-012 Arabidopsis thaliana. ; 6661-NUT-81 18-JUL-1999 

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324 CTTGGAAACTGGAGAATCAGTAGCCATTAAGAAGGTTTTGCAAGATCGCCGTTATAAAAA 383
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Arabidopsis thaliana DNA fragment SEQ ID NO: 17866.

Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.

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99US-0128234P.

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8-JUN-1999

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                                                       TGAGACGTTGTATCGAGTTCTGAAACATTATAGTAGTGCAAACCAAAGAATGCCTCTTGT
                                                                    CTATGTCAAACTTTACACATACCAAATCTTCAGAGGCTTGGCTTATATCCATACTGCTCC
                                                                                                                                                    TGGTGTCTGCCACAGAGATGTGAAACCACAAAATCTTTTGGTTGATCCCCTCACCCATCA
                                                                                                                                                                    AGTCAAAATCTGTGACTTTGGCAGTGCGAAACAGCTCGTTAAAAGGTGAACCAAACATTTC
                                                                                                                                                                                                          TTACATCTGCTCACGATTCTACCGTGCACCCCGAGCTCATATTTGGTGCCACTGAGTACAC
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                                                                                                                                                                                                                                                                                                                                                             GATAAAGGCCCATCCCTGGCACAAGATCTTCCACAAAAGGATGCCCCCAGAAGCGGTTGA
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CCGAGAGTTGCAATTAATGCGACTAATGGACCATCCAAATGTGGTTTCCTTGAAGCATTG
                  CTTCTTTTCGACTACAGAGAAGACGAGCTTTTCTTGAACTTGGTTATGGAGTATGTCCC
                               CTATGTTAAACTTTACAGTTATCAGATCTTCCGGGGACTTGCTTACATTCACAGTTGCCC
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The present sequence is a full-length cDNA encoding GmPK-3, a novel soybean protein kinase stress-related polypeptide (PKSRP). The cDNA was identified on the basis of homology to Physcomitrella patens PK-3 (see ACC57962) and PK-10 (see ACC57966) sequence. GmPK-3 is an example of PKSRPs of the invention that are important for modulating a plant's response to environmental stress. Over-expression of PKSRP coding nucleic acids in a plant results in the plant's increased tolerance to environmental stress. Transgenic monocot and dicot plants are provided that show increased tolerance to high salinity, drought and low
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GmPK-3; protein kinase stress-related polypeptide; PKSRP; enz transgenic plant; plant; stress tolerance; drought tolerance; salt tolerance; cold tolerance; soybean; gene; ss.
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protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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Length 1567; Indels Score 705.6; DB 3; Pred. No. 5.1e-186; 0; Mismatches 259; 9905-015377099905-015377099905-01547889905-01547889905-01547889905-01556599905-01556599905-01577399905-01577399905-01577399905-01592399905-01592389905-01592389905-01592389905-01592389905-01592389905-01592389905-01592389905-01592389905-016098149905-016098149905-016098189905-016098189905-016098189905-016098189905-016098189905-016098189905-016098189905-016098189905-01609818-99US-0152363P 40.6%; il Similarity 76.9%; 861; Conservative 10-SEP-1999; 10-SEP-1999; 113-SEP-1999; 12-SEP-1999; 12-SEP-1999; 12-SEP-1999; 12-SEP-1999; 13-OCT-1999; 13-OCT-1999; 13-OCT-1999; 14-OCT-1999; 13-OCT-1999; 14-OCT-1999; 13-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 15-OCT-1999; 16-OCT-1999; 17-OCT-1999; 18-OCT-1999; Query Match Best Local Si Matches 861 

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              CTTTATACCGGGTTTTTGAGGCACTATACTAGTTCTAATCAGAGGAGGGATTTTCTATG
                                     TCCCCGGAGAAATGCTGTGGATCAGCTCGTGGAAATTATTAAAGTTCTTGGTACAAA
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223 CTGCTGCTGTTGTTGATGGACATGATCAAGTCACTGGTCATATTATTTCCACCACAATCG 168 CTGGTTCTATGATTGAAGGGAGTGATCCGGTCACAGGCCATATAAATCTCGACAATGG

Query Match
38.9%; Score 676.8; DB 3; Length
Best Local Similarity 75.3%; Pred. No. 5.8e-178;
Matches 843; Conservative 0; Mismatches 277; Indels

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transgenic plant; plant; stress tolerance; drought tolerance;
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The present sequence is a full-length cDNA encoding GmPK-1, a novel soybean protein kinase stress-related polypeptide (PKSRP). The CDNA was identified on the basis of homology to Physcomitrella patens PK-3 (see ACC57962) and PK-10 (see ACC57966) sequence. GmPK-1 is an example of PKSRPB of the invention that are important for modulating a plant's response to environmental stress. Over-expression of PKSRP coding nucleic acids in a plant results in the plant's increased tolerance to environmental stress. Transgenic monocot and dicot plants are provided that show increased tolerance to high salinity, drought and low
                                                                                                                                                                                                                                                      New protein kinase stress-related polypeptide coding nucleic acid, useful for producing transgenic plants with an increased tolerance to an environmental stress, e.g. high salinity, as compared to a wild type variety of the plant.
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09-NOV-2001; 2001US-0346096P.
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-- Tocal Similarity
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The invention relates to protein kinases, especially calcium-dependent phosphorylase kinase (CDPK) and glycogen synthase kinase-3 (GSK-3). The polypeptides having GSK activity can be expressed by standard recombinant cathology. The polymucleotides encoding the polypeptides are useful for including cDNAs and genes encoding homologous proteins from the same or cisolating cDNAs and genes encoding the monological screening of cDNA expression cother plant species, for immunological screening of cDNA expression cother plant species, for immunological screening of cDNA expression synthase kinase polypeptides are present at higher or lower levels than command or in cell types or developmental stages in which they are commanded to mormally found. The polynucleotides are also useful as probes for genetically and physically mapping the genes that they are part of, and as markers for traits linked to those genes. The polypeptides are useful for altering the level of expression of GSK-3 in a transformed host cell. The present sequence represents a wheat GSK-3 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 649.2;
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The present invention describes kinase polypeptides (I) such as a calcium

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cdependent phosphorylase kinase polypeptide comprising a sequence of 101, 623, 157 or 111 (see ABP53629 to ABP5362) amino acids, and a glycogen synthase kinase polypeptide comprising all or a portion of a sequence of 410, 105, 399 or 402 (see ABP53631 to ABP53636) amino acids. (1) is useful for immunological screening of CDNA expression libraries, and for preparing antibodies against the polypeptides, where the antibodies would be useful for detecting (1) in situ or in vitro, in cell extracts.

CC buseful for detecting (1) in situ or in vitro, in cell extracts.

CC Nucleic acids (11) encoding (1) can be used to isolate CDNAs and genes encoding homologous proteins from the same or other plant species. (11) can also be used for creating transgenic plants in which (1) is present developmental stages in which they are not normally found. (11) are useful as probes or primers. The polymodicatides may be used as probes or primers. The polymodicatides may be used as part of and used as markers for traits linked to those genes that they are a part of an used in plant breeding in order to those genes. The information can be used in plant breeding in order to develop lines with desired

CC phenotypes. The present sequence encodes a glycogen synthase kinase from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1673 BP; 419 A; 421 C; 408 G; 424 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 GATGGACATGATCAGTCACTGGTCATATTATTTCCACCACAATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch
37.4%; Score 649.2; DB 6;
al Similarity 74.9%; Pred. No. 3e-170;
813; Conservative 0; Mismatches 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention
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	) AACTTC 1234	1229	С
	/ AGCTTC 1322	1317	δ
1228	GCCTCTCCAGAGCTCATCAACAGGCTTGTTCCGGAACATGTTCGACGGCAAAATGGCCCC	1169	qa
1316	TCATCACCTGAACTGGTCAAGTTGATTCCAGACCATATCAAGAGACAATTGGGTCTA	1257	ò
1168	CGCTTGCCGAATGGCCGCCCATTCCCTCTCTTTTAAACTTCAAACTGAACGAAC	1109	qa
1256	CGTTTACCAAATGGACGCCTCTCCCGCCTCTCTAACTTCAAACAAGAAGTAGCTGGA	1197	ò
1108	IGCACTGCTCTTGATGCATGTGCACATTCCTTTGATGAGCTACGTACG	1049	qa
1196	TGCACAGCGCTCGAAGCTTGTGCACCATCCGTTCTTTGATGAACTCCAGAGAACGCT	1137	ò
1048	ATGCCCGCTGAAGCTATAGATCTTGCCTCCCGCCTTCTCCAGTATTCACCAAATCTACGT	686	qa
1136	ATGCCCCCAGAAGCGGTTGATTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGA	1077	ò
988	ACCAGTICAGGITICCICAGATIAAGGCICAICCITGGCACAAGAITTICCACAAGAGA	929	qq
1076	A CAGATITICAAGTICCCACAGATAAAGGCCCATCCCTGGCACAAGATCTICCACAAAAGG	1017	ò
928	ATTATCAAGGTTCTTGGTACTCCAACCCGTGAGGAATTCGGTGCATGAACCCCCAACTAT	869	QG
1016	ATTATTAAAGTTCTTGGTACACCCAACTCGAGAAATCCGTTGTATGAATCCCAACTAC	957	ò

Search completed: June 23, 2005, 11:47:02 Job time: 1367.08 secs

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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

Run on:

June 23, 2005, 10:21:17; Search time 422.305 Seconds (without alignments) 6734.116 Million cell updates/sec

X94939 1738 Perfect score: Sequence:

IDENTITY NUC Scoring table:

Gapop 10.0 , Gapext 1.0

1202784 seqs, 818138359 residues Searched:

2405568 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Patents NA:\* Issued Database

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/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		•			SOMMAKIES		
Result No.	Score	Query Match	/ 1 Length	DB	aı	Description	
-	734.6	42.3	3 1636	-	US-09-578-194-6	Sequence 6, Appli	
8	649.2		٦	ო	09-347	15,	
٣	649.2	٠	-	4	US-09-854-731-15	Sequence 15, Appl	
4	590	33.5	9 1814	m	US-09-347-801-9	9,	
Ŋ	590	33.5	1814	4	US-09-854-731-9	6	
9	530.4	30.5	5 1429	ო	US-09-347-801-13	13	
7	530.4	30.5	5 1429	4	US-09-854-731-13	13,	
۵	399.6	23.0	0 1952	4	US-09-566-921-24	N	
ō	399.6	23.0	0 2154	ო	US-09-488-856A-3	3,	
10	393.2	ς.		~	US-08-602-264A-1	7	
11	393.2	22.6		ო	US-08-461-018A-1	٦,	
12	393.2	22.6	6 2088	m	US-09-216-958-1	Sequence 1, Appli	
13	391.6	22.5		ო	US-09-489-765A-3	'n	
14	391.6	22.	5	4	US-09-016-434-1414	141	
15	391	22.	5 1972	~	US-08-602-264A-2	7	
16	391	22.		ო	US-08-461-018A-2	7	
17	391	22.	5 1972	ო	US-09-216-958-2	Sequence 2, Appli	
18	286.4	16.5		4	US-09-248-796A-4396	43	
19	163	9.	===	4	US-09-313-294A-6825	6825,	
20	142.4	80	C)	4	US-09-313-294A-5874	5874,	
21	142.2	8	~	4	US-09-313-294A-2895		
22	129.8	7	17	4	US-09-248-796A-4397	4397,	
23	115.6	9	7 272	4	US-09-313-294A-6721	672]	
24	107	9	~	e	US-09-347-801-11	11, Ap	
25	107	9	2 584	4	US-09-854-731-11	11,	
56	106.4	6.	_	4	-09-313-294A-1	170	
27	101	5.	8 479	7	US-08-602-264A-13	13,	

Sequence 13, Appl Sequence 13, Appl	4 (1:	Sequence 11, Appl Sequence 5, Appli	9,0	Sequence 3, Appli Sequence 1, Appli	Sequence 11493, A	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Seguence 1, Appli	Seguence 1, Appli	Sequence 1, Appli	Sequence 4276, Ap	Seguence 4296, Ap
US-08-461-018A-13 US-09-216-958-13	US-09-623-034-1	US-09-6/1-050-11 US-09-671-050-5	US-09-671-050-9	US-09-6/1-050-3 US-08-837-593-1	US-09-270-767-11493	US-08-176-620A-1	US-08-463-862-1	US-08-461-985-1	US-08-458-887-1	US-08-932-787B-1	US-08-932-012C-1	US-08-888-818C-1	US-09-949-016-4276	US-09-248-796A-4296
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479	1725	945 972	1041	1068	438	1747	1747	1747	1747	1747	1747	1747	3823	666
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101	99.2	91.6	88.6	83.8 83.8	78.8	78	78	78	78	78	78	78	75.6	73.2
28 29	30	32	33	3.4	36	37.	38	39	40	41	42	43	44	45

## ALIGNMENTS

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AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and Kreis, M. TITLE: Three New cDNAs Related to SGG/GSK-3 ( Shaggy/Glycogen Synthase Kinase-3) TITLE: from Arabidopsis thaliana ( Accession No. 6822139 X94938, x94939 and X99696) TITLE: 008)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: mRNA
LOCATION: (1)...(1636)
OTHER INFORMATION: strain Columbia ecotype
OTHER INFORMATION: taxon:3702
OTHER INFORMATION: tissue type leaves
OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots
PUBLICATION INFORMATION:
AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 CGCCATGGCTGATGATAAGGAGATGCCTGCTGCTGTAGTTGATGGACATGATCAAGTCAC
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42.3%; Score 734.6; DB 4; Length
Best Local Similarity 77.5%; Pred. No. 8.2e-200;
Matches 890; Conservative 0; Mismatches 259; Indels
                                                                                                                                                                                                                               APPLICANT: Sudwestdeutsche Saatzucht-SWS
APPLICANT: Advanta Seeds B.V.
FITLE OF INVENTION: Modulation of Storage Organs
FILE REFERBNCE: 026-1
CURRENT APPLICATION NUMBER: US/09/578,194
CURRENT FILING DATE: 2000-05-24
NUMBER OF SEG. 10 NOS: 6
SOFTWARE: Patent In version 3.1
FENCINE OF SEG. 10 NOS: 10 NO
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DATABASE ACESSION NUMBER: genbank/X94938
DATABASE ENTRY DATE: 1996-02-13
RELEVANT RESIDUES: (1)..(1636)
5-09-578-194-6
Sequence 6, Application US/09578194
Patent No. 6822139
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Arabidopsis sp.
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL: Plant Physiol.
VOLUME: 113
ISSUE: 1
PAGES: 306-306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-578-194-6
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256

197 CGGTCACATAATTTCTACTACAATTGGAGCAAAAATGGTGAACCTAAACAGACCATAG

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837 TTTGGTGCCACTGAGTACACATTCTATTGATATCTGGTCTGCTGGTTGTGTTCTTGCT
749 TTTGGTGCAACTGAATATACAACTTCAATAGACATATGGTCAGCTGGATGTGTTCTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                       Length 1673,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                      37.4%; Score 649.2; DB 3; 74.9%; Pred. No. 2.4e-175; tive 0; Mismatches 273;
                            Sequence 15, Application US/09347801
Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allen, Steve
TILE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Triticum aestivum
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.4
Best Local Similarity 74.9
Matches 813; Conservative
                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: unsure
; LOCATION: (1349)
US-09-347-801-15
               US-09-347-801-15
                                                                                                                                                                                                                                                         SEQ ID NO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATAAAGGCCCATCCCTGGCACAAGATCTTCCACAAAAGGATGCCCCCAGAAGCGGTTGA 1096
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 376
                 436
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 TTACATGGCGGAGCGAGTTGTTGGTACAGGCTCGTTCGGGATCGTTTTCCAAGCAAAATG
                                                                                    317 CTIGGAAACTGGAGAATCAGTAGCCATTAAGAAGGTTTTGCAAGATCGCCGTTATAAAAA
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                                                                  ITTGCAAGATAGAAGATACAAGAA
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Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allan, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
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                                                                                                             ACAGATTCCAAGATACCCACAGATAAAGGCCCCATCCCTGGCACAAGATCTTCCACAAAAGG
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APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REPERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/092,438
PRIOR PILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 15
LENGTH: 1673
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Patent No. 6794561
GENERAL INFORMATION:
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; LOCATION: (1349)
US-09-854-731-15
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US-09-854-731-15
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                                                                                                                                                                                                                                                                                                                              GGACGCCTCTCCCCCCTCTCCAACTTCAAAC 1242
                                                                                                                                                                                                                                                                                                                                                              ; Sequence 9, Application US/09854731
; Patent No. 6794561
; GRNERAL INFORMATION:
APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; RIGH FILING DATE: 1019 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
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ORGANISM: Zea mays
US-09-854-731-9
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US-09-854-731-9
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Best Local Similarity 72.5%; Pred. No. 2.3e-158;
Matches 764; Conservative 0; Mismatches 290; Indels
                    CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 9
REFERENCE: BB-1171
                                                                                                                                                                                                                 LENGTH: 1814
; TYPE: DNA
; ORGANISM: Zea maye
US-09-347-801-9
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Pred. No. 2.3e-141;
0; Mismatches 318; Indels
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Best Local Similarity 69.5
Matches 733; Conservative
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Patent No. 6262345
GENERAL INFORMATION:
TENDERAL INFORMATION:
APPLICANT: Allen, Steve
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT FILING DATE: 1999-07-02
EARLIER FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER PILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
LENGTH: 1429
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ORGANISM: Glycine m.
FEATURE:
NAME/KEY: unsure
LOCATION: (1202)
FRATURE:
NAME/KEY: unsure
LOCATION: (1237)
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US-09-566-921-24

; Sequence 24, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.;
; APPLICANT: Edwards, Carla M.;
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE;
; FILE REPERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SEQ ID NO 24
; SEQ ID NO 24
; LENGTH: 1952
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ORGANISM: Homo sapiens
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                                                                                                                                          1169 CTTGGACGCCCTTTCCTTTGGACGAATTCCGNGATCCAAATCCTCGCTTGCCAAATGG 1228
   1049 ACAGATTAAAGCACATCCATGGCACAAGATCTTCCATAAGCGCATGCCTCCAGAGGCTGT 1108
                                      TGATTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCACAGGCGCTCGAAGC 1153
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llarity 69.5%; Pred. No. 2.3e-141;
Conservative 0; Mismatches 318;
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                                                                                                                                                                                                                             1229 GCCGATCCNTCCAACAACTATTAATTCAAACCCA 1262
                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/09854731
Patent No. 6794561
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Allen, Steve
TITLE OF INVENTION: Plant Protein Kinases
FILE REPERBNCE: BB-1171
CURRENT FILING DATE: 2001-05-14
PRIOR PILING DATE: July 10, 1998
NUMBER: OF SEQ ID NOS: 23
SEQ ID NO 13.
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US-09-854-731-13
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                                                                 23.0%; Score 399.6; DB 4; Length 1952; 65.0%; Pred. No. 8e-104;
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           NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6682888 234735.15
                                                                                            0; Mismatches 329;
                                                                                          623; Conservative
                                                                              Similarity
                           , OTHER INFORM
US-09-566-921-24
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APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Madeline M. Butler
APPLICANT: Jacqueline Myatt
TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXPR
FILE REFERENCE: RTS-0115
CURRENT APPLICATION NUMBER: US/09/488,856A
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
LENGTH: 2154
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                                                                                                                                                                                                                                                                                                                                                                                     Score 399.6; DB 3;
Pred. No. 8.4e-104;
0; Mismatches 329;
                           Sequence 3, Application US/09488856A
Patent No. 6316259
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.0%;
Best Local Similarity 65.0%;
Matches 623; Conservative
                                                                                  Brett P. Monia
                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (92)...(1543)
US-09-488-856A-3
                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 9
US-09-488-856A-3
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TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR

TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
TITLE OF INVENTION: 1au-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 805 Fifteenth LIND & PONACK STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington SIP: 20005
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MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 144 mb.
COMPUTER: ISM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/602,264A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: February 20, 1996
CLASSIFICATION: 514
RIOR APPLICATION DATA:
PILING DATE: MACH 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN N. Cheek, Jr.
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
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Patent No. 5837853
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
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ORIGINAL SOURCE:
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US-08-602-264A-1
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                                              TCCTCTTACTCATCAAGTCAAAATCTGTGACTTTGGCAGTGCGAAACAGCTCGTTAAAGG
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Patent No. 6248559
GENERAL INFORMATION:
APPLICANT:
ARIDINO:
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STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
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US-09-216-958-1
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APPLICANT: Akihiko TAKASHIMA et al.
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEBE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
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                                                                                                                                                                                                                                           SITEMENT OND FILEGEBLEN STREET, N.W., #
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: 1.44 mb
COMPUTER: I.MA COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,018A
FILING DATE: June 5, 1995
CLASSIFICATION NATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
METELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2008 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 637; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.5%; Score 391.6; DB 3; Best Local Similarity 63.2%; Pred. No. 1.3e-101; Matches 636; Conservative 0; Mismatches 364;
                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09489765A
Patent No. 6323029
GENERAL INFORMATION:
APPLICANT: Madeline M. Butler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (40).
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US-09-489-765A-3
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                                                                                                                                                                                                                                                                                           Query Match 22.6%; Score 393.2; DB 3; Best Local Similarity 63.3%; Pred. No. 5.7e-102; Matches 637; Conservative 0; Mismatches 363;
                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA to genomic RNA ORIGINAL SOURCE:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
                                                                                          INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2008 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                        ORGANISM: human being
                                                                                                                                                                                                                                            ;
US-09-216-958-1
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APPLICANT: Robert McKay
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRESS
FILE REFERENCE: RTS-0124
CURRENT APPLICATION NUMBER: US/09/489,765A
CURRENT FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 85

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CCCAGAAGCGGTTGATTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCAC 1141
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                                                                                                                                                                                                                                                                                                                    Score 391.6; DB 4;
Pred. No. 1.3e-101;
0; Mismatches 364;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEPHONE: (650) 845-0556
INFORMATION FOR SEQ ID NO: 1414:
SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 952936
US-09-016-434-1414
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Best Local Simil
Matches 636; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCAGAAGCGGTTGATTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCAC
                                                   TGAACCAAACATTTCTTACATCTGCTCACGATTCTACCGTGCACCCGAGCTCATATTTGG
                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1262 ACCTGAACTGGTCAACAAGTTGATTCCAGACCATATCAAGAGACAA 1307
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PA-0002 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1414, Application US/09016434
Patent No. 6500938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAWE: Zeller, Karen J.
REGISTRATION NUMBER: 37,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: PALO ALTO STATE: CALIFORNIA
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US-09-016-434-1414
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TGGCGATAAAGAAGGTTTTGCAAGATAGAAGATACAAGAACCGAGAACTTCAGTTGATGC
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                                                                                                                                                                                                                                                                                                                      504 AGAAAGATGAGGTCTACCTTAACCTGGTGCTGGACTATGTTCCGGAAACAGTGTACAGAG
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                                          GTGTGATGGATCATCCGAATGTGGTTTGTTTGAAGCATTGCTTCTTTTCGACTACAG---
                                                                                                                                                                                     GAAAGCTAGATCACTAACATAGTCCGATTGCGGTATTTCTTCTACTCGAGTGGCGAGA
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Job time : 426.305 secs
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Patent No. 5837853

GENERAL INFORMATION

APPLICANT: Akihiko TAKASHIMA et al.

APPLICANT: Akihiko TAKASHIMA et al.

TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR

TITLE OF INVENTION: AAZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE

TITLE OF INVENTION: LAU-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: WENDEROTH, LIND & PONACK

STREET: 805 Fifteenth Street, N.W., #700

COUNTRY: D.C.

ZIP: Z0005

COMPUTER READABLE FORM:

MEDIUM TYPE: 01skette, 3.5 inch,

MEDIUM TYPE: 01skette, 3.
                                                    1029 ACCACTGGAAGCTTGTGCACATTCATTTTTGATGAATTACGGGACCCAAATGTCAAACA 1088
                                                                                                                                                                        1089 TCCAAATGGGCGAGACACACCTGCACTCTCAACTTCACCACTCAAGAACTGTCAAGTAA 1148
      AGCGCTCGAAGCTTGTGCACATCCGTTCTTTGATGAACTCAGAGAACCAAACGCTCGTTT 1201
                                                                                                                             1202 ACCAAATGGACGGCCTCTCCCGCCTCTTCAACTTCAAACAAGAAGTAGCTGGATCATC 1261
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                                                                                                                                                                                                                                                                                                                      1149 récaceréréseracearcerrariéerecréarseressarréa 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: MARCH 2, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1972 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: rat
US-08-602-264A-2
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-08-602-264A-2
   1142
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June 23, 2005, 10:41:47; Search time 1872.84 Seconds (without alignments) 5800.480 Million cell updates/sec
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/ptodata/2/pubpna/US10H_PUBCOMB.seg:*
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GenCore version 5.1.6
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                                                                                                                                                                                                                                                                       6067389 seqs, 3125258755 residues
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Maximum Match 100%
Listing first 45 summaries
                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                       IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                           Sequence:
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                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 1 2 3 3 4	Score 1431.6 1099.8 1099.8 1058.4 759.2	•	Length 1490 1143 1143 1143 1979	21 US 11 US	DB ID.  21 US-10-477-687-12  9 US-09-938-842A-875  11 US-09-928-842A-875  16 US-10-292-408-15  18 US-10-425-459-57990	Description Sequence 12, Appl Sequence 875, App Sequence 15, Appl Sequence 15, Appl Sequence 12807, A
7	750.2	43.2		18	US-10-424-599-67987	Sequence 67987, A

Sequence 6, Appli Sequence 25, Appl Sequence 67989, A	22987	21, App 26109, 24168,	~ ~ ~ ~ ~ ~	22299, 148434, 13850, 17458,	Sequence 32310, A Sequence 32310, A Sequence 3522, A Sequence 3772, Ap Sequence 32862, A Sequence 30667, A	11127 26106 14202 10030 13360	23 5 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
US-10-764-138-6 US-10-292-408-25 US-10-424-599-67989	29872 22950 32993	1 610 416	US-10-437-963-98579 US-10-425-115-22953 US-09-854-731-15 US-10-425-114-34808	US-10-425-114-22299 US-10-425-114-22299 US-10-425-115-148434 US-10-425-114-13850 US-10-425-114-17458	US-10-425-115-32308 US-10-425-115-32310 US-10-425-114-3522 US-10-425-114-32862 US-10-425-114-32662	US-10-425-115-111277 US-10-425-114-26106 US-10-767-701-14202 US-10-425-114-10030 US-10-424-599-133605 US-10-739-930-4849	US-10-437-963-9996 US-09-938-842A-2358 US-10-932-408-2 US-10-425-114-9488 US-10-424-14-9488 US-10-767-701-14423
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## ALIGNMENTS

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US-10-477-687-12

US-10-477-687-12

Sequence 12, Application US/10477687

Publication No. US20050049397Al

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Choc. Sunghwa

APPLICANT: Tax, Frans

TILLE OF INVENTION: DWR12 and Mutants Thereof

FILE REFERENCE: 1166-075531

CURRENT APPLICATION NUMBER: US/10/477,687

CURRENT APPLICATION NUMBER: US/10/477,687

CURRENT APPLICATION NUMBER: US/10/477,687

CURRENT APPLICATION NUMBER: US/00/20133

PRIOR PILING DATE: 2002-05-15

PRIOR PILING DATE: 2001-05-16

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 1490

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: A DWF12 CDNA

GORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: A DWF12 CDNA

US-10-477-687-12

Query Match

Best Local Similarity 98.0%; Pred. No. 0;

Matches 1460; Conservative 0; Mismatches 29; Indels 1; Gaps
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; Sequence 875, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Harper, Jeff
; APPLICANT: Wang, Xun
; APPLICANT: SAME, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFREENCE: SCRIPAIOO-09-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR PILING DATE: 2001-08-24
; PRIOR PILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: S379
; SEQ ID NOS: S379
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RESULT 3
US-09-938-842A-875
Sequence 875, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff

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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: And, Tong
ITILE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPRENCE: SCRIP1300-3
CURRENT PRILICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/224,647
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-6-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 875
LENGTH: 1143
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Pred. No. 7.5e-307;
0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-875
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ilarity 97.6%;
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US-10-292-408-15

is Sequence 15, Application US/10292408

is General INFORMATION:

is APPLICANT: VAN THELEN, NOCHA

is APPLICANT: DA COSTA E SILVA, OSWALDO

is APPLICANT: CHEN, RUOYING

is TITLE OF INVENTION: OF USE IN PLANTS

is FILE REFERENCE: 16313-0178

is CURRENT APPLICATION NUMBER: US/10/292,408

is CURRENT PILING DATE: 2002-11-12

is PRIOR FILING DATE: 2001-11-09

is NUMBER OF SEQ ID NOS: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 15
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                     TACAAGAATCGTGAACTGCAGTTAATGCGTGTGATGGATCATCCAAATGTGATCTCTTTG
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Sequence 67990, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
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PUBLICATION NO. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jindedong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Papaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 12807

LENGTH: 1726
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44.2%; Score 768.6; DB 18; Length
Best Local Similarity 77.0%; Pred. No. 6.5e-211;
Matches 936; Conservative 0; Mismatches 279; Indels
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APPLICANT: Kovalic David K
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APPLICANT: Kovalic David K
APPLICANT: Cao Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 67987
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Pred. No. 1.4e-205;
0; Mismatches 303;
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 75.5%;
Matches 932; Conservative
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement . FILE REFERENCE: 38-21(53223) B CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
ESEQ ID NO 67990
LENGTH: 1979
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Pred. No. 3.7e-208;
0; Mismatches 268;
                                                                                                                                                                                                  PAT_MRT3847_32408C.1
                                                                                                                                                                                                ) OTHER INFORMATION: Clone ID: US-10-424-599-67990
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.4%;
Matches 920; Conservative
                                                                                                                                              TYPE: DNA
ORGANISM: Glycine max
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                                                                                                                  GTAGTGCAAACCAAAGAATGCCTCTTGTCTATGTTAAACTTTTACAGTTATCAGATCTTCC
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Sequence 6, Application US/10764138
Publication No. US20050081266A1
GENERAL INFORMATION:
APPLICANT: Sudwestdeutsche Saatzucht-SWS
APPLICANT: Advanta Seeds B.V.
TITLE OF INVENTION: Modulation of Storage Organs

RESULT 8 US-10-764-138-6

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TYPE: DNA
ORGANISM: Arabidopsis sp.
PEATURE:
NAME/KEY: mRNA
LOCATION: (1)..(1636)
OTHER INFORMATION: strain Columbia ecotype
OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots
OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots
PUBLICATION INFORMATION:
AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and Kreis, M.
TITLE: Three New CDNAS Related to SGG/GSK-3 ( Shaggy/Glycogen Synthase Kinase-3)
TITLE: Three New CDNAS Related to Accession No. X94938, x94939 and X99696) ( PGR97-TITLE: 008)
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VOLUME: 113
ISSUE: 306-306
DATE: 1997-01-01
DATABASE ACCESSION NUMBER: genbank/X94938
DATABASE ENTRY DATE: 1998-02-13
RELEVANT RESIDUES: (1)..(1636)
FILE REFERENCE: 026-1
CURRENT APPLICATION NUMBER: US/10/764,138
CURRENT FILING DATE: 2004-01-23
PRIOR PILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
LENGTH: 1636
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Sequence 124766, Application US/10424599;
Sequence 124766, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: PLANTS
SOUTH OF THING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 144786
LENGTH: 2519
TYPE: DNA
ORGANISM: Glycine max
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 32-21(5):23.9

CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

LENGTH: 1744
TAGGCTCATCCCAGAGCATATTAGGCGGCAGATGGGTCTCAGCTTCCCGCATTCTGCCGG 1295
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                                CTGAAGCATTGTTTCTTTTTCAACTACAAGTACAGATGAGCTTTTTTCTTAATTTTGGTGATG
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                                                                                            1397 AGCCACAAGGTC 1408
                                                                                                                         1356 CAACAGAAGGGC 1367
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Best Local Similarity 73.5
Matches 949; Conservative
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ORGANISM: Glycine max
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RESULT 12
US-10-437-963-29872/C
US-10-437-963-29872/C
Sequence 29872, Application US/10437963
Sequence 29872, Application No. US20040123343A1
SEQUENCE 10 No. US20040123343A1
SEPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Barbark, Nai
APPLICANT: Barbark, Brad
APPLICANT: Howele and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT PRILIG DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
SEQ ID NOS: 204966
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Pred. No. 8.2e-187;
0; Mismatches 276;
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Matches 851, Conservative
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                                                                                                                    3;
                                                                              Length 2519;
                                                                              Query Match
39.6%; Score 688.2; DB 18; Length
Best Local Similarity 76.5%; Pred. No. 1.5e-187;
Matches 882; Conservative 0; Mismatches 268; Indels
                      i, OTHER INFORMATION; Clone ID: PAT_MRT3847_83691C.1
US-10-424-599-124786
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Application David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated ITILE OF INVENTION: Plants
FILE REPERENCE: 38-21(53222)B
CURRENT FILING NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-44-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 22950
                                                                                                  GAAACAGCTCGTTAAAGGTGAACCAAACATTTCTTACATCTGCTCACGATTCTACCGTGC
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                    CTTCCGGGGACTTGCTTACATTCACAGTTGCCCCGGGAGTTTGTCACAGAGATCTAAAGCC
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; OTHER INFORMATION: Clone ID: MRT4577_120933C.1
US-10-425-115-22950
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ORGANISM: Zea mays
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                                                                      CTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGGTCATATTATTTCCACCACAATCG
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Best Local Similarity 75.4%;
Matches 844; Conservative
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                                                                                                                                                                                                                                                                                              898 TAATAAAGGTTCTTGGTACTCCCAACGCGCGAGGAAATCCGATGTATGAATCCAAACTACA 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/10292408
Publication No. US20030182692A1
GENERAL INFORMATION:
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: CHEN, RUOYING
TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS
TITLE OF INVENTION: OF USE IN PLANTS
FILE REFERENCE: 16313-0178
CURRENT APPLICATION NUMBER: US/10/292,408
CURRENT FILING DATE: 2002-11-12
CURRENT FILING DATE: 2002-11-12
PRIOR FILING DATE: 2001-11-09
                                                                                                                       838 AGCTGCTTCTTGGCCAGCCTCTCTTCCCTGGTGAAAGTGCTGTGGATCAGCTTGTTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 GATAAGGAGATGCCTGCTGTAGTTGATGGACATGATCAAGTCACTGGTCATATTATT
                   AAGGIGAACCAAACATITCTIACATCTGCTCACGAITCTACCGTGCACCCGAGCTCATAT
                                                     718 AAGGTGAAGCAAACATATCATATGTTCACGTTATTACCGTGCTCCAGAGCTCATAT
                                                                                                                                                                                                                                                                                                                                                 Query Match 38.4%; Score 667.6; DB 16; Length 1499; Best Local Similarity 75.5%; Pred. No. 9.9e-182; Matches 829; Conservative 0; Mismatches 269; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1318 GCTTCTTGAATCAATCTGGAACTTA 1342
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SEQ ID NO 21
LENGTH: 1499
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CORGANISM: Glycine max
US-10-292-408-21
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US-10-292-408-21
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                                                                                                                                                                                                      Sequence 32993, Application US/10425114
; Sequence 32993, Application No. USZ0040034888A1
; Publication No. USZ004003488BA1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION WUBBER. US/10/425,114
; CURRENT PILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
243 AAGAAGTAGCTGGATCATCACCTGAACTGGTCAACAAGTTGATTCCAGACCATATCAAGA 1302
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                     509 AGGAACTAGCAAAATGCCTCCCCGGAGCTCATCAACAGGTGATCCCAGACCATGCTAGGC 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCAAAACAGACAATTAGTTACATGGCGGAGCGAGTTGTTGGTACAGGCTCGTTCGGGA 357
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                                                                               1303 GACAATTGGGTCTAAGCTTCTTGAATCAATCTGGAACTTA 1342
                                                                                                  ; OTHER INFORMATION: Clone ID: UC-ZMFLMO17050F06_FLI
US-10-425-114-32993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Zea mays
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LENGTH: 1887
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                      | CGAGTTGTTGGTACAGGCTCGTTCGGGATCGTTTTCCAAGCAAAATGTTTGGAGACTGGA
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Search completed: June 24, 2005, 08:33:16 Job time: 1875.84 secs



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OM nucleic - nucleic search, using sw model

Run on:

June 23, 2005, 10:16:02; Search time 8631.11 Seconds (without alignments) 7664.793 Million cell updates/sec

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

34239544 seqs, 19032134700 residues Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	9	Query	Guery Match Length DB	ä	Ę	TO STATE OF THE PARTY OF THE PA	
				3			;
-	702.4	40.4	1409	٣	CNSOABFT	BX815323 Arabidops	8di
7	700.8	40.3	1461	٣	CNSOABLV	BX817800 Arabidops	8d
m	6.969	38.9	1745	٣	AY106255	AY106255 Zea mays	ĘD.
4	663	38.1	1197	σ	CL957492	CL957492 OSIFCC000	00
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y	630.6	36.3	689	-	AV821208	AV821208 AV821208	œ
7	623.4	35.9	1961	m	AY103545	AY103545 Zea mays	ĆΩ
<b>&amp;</b>	611.8	35.2	1638	ო	CNS09YSF	BX831446 Arabidops	gd.
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10	600.4	34.5	665	9	CA781809	CA781809 051B01AF	Eų,
11	591.6	34.0	1752	ო	AY108486	AY108486 Zea mays	8
12	585.4	33.7	1870	m	CNSOADOL	BX813745 Arabidops	gd.
13	581.4	33.5	2295	0	CL964803	_	11
14	580.2	33.4	887	9	CD574542	CD574542 UCRPT01	0
15	579.8	33.4	924	7	CK266410	CK266410 EST712488	88
16	577	33.2	1604	m	CNS0A4PT	BX823861 Arabidops	80
17	571.4	32.9	932	7	CV290871		Sm.
18	570.4	32.8	1275	6	CL963186	CL963186 OSIFCC008	90
19	569.6	32.8	910	7	CK290108	CK290108 EST752830	30
20	567.2	32.6	829	9	CB971865	_	اي
21	558.6	32.1	1667	ന	CNSOA5F6	BX823376 Arabidops	sđ
c 22	550.8	31.7	266	Н	AV535992	AV535992 AV535992	ر اي
23	545.4	31.4	790	7	CO107864	CO107864 GR Eb003	03
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CK286080	CNSOADRT	CNS0A425 .	CK286429	CB894470	CK289285	CK290066	AV526323	AV527913	C0120041	CK296951	CNSOASFS	CK319050	AV441767	C0083924	CF208184	AV821730	BM779604	CK273361	CK283056	CK266742
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## ALIGNMENTS

CNSOABFT Arabidopsis GSLTLS51ZG03 Arabidopsis BX815323	BX815223.1 GI:42471412 HFC; GSLF. CDNA Arabidopsis thaliana (thale cress) Arabidopsis thaliana Arabidopsis thaliana Arabidopsis thaliana Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	1 (bases 1 to 1409) Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation Unpublished 2 (bases 1 to 1409) Genoscope. Direct Submission	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - The be sequences are based on single pass reads.  Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.  Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.  URCY INRA : Clepet C., Caboche M.  Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein	
RESULT 1 CNSOABFT LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE	COMMENT	FEATURES BOUT CE

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              /tissue type="Adult vegetative tissue"
/plasmid="pCMVSPORT_6"
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0; Mismatches 261;
clone="GSLTLS51ZG09"
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/gene="At1g06390"
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Best Local Similarity 76.7%;
Matches 859; Conservative
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EWRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads .

The sequences are based on single pass reads .

The sequences are based on the light of Castelli of Echnologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli of C. Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepter C., Caboche M. Wincker P., Menard M., Cruaud C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) . 5 prime and 3 prime are assembled with Phrap. Intp://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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(Dasses 1 to 1461)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M. Whole Genome Sequence Comparisons and 'Pull-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Arabidopsis thaliana Full-length CDNA Complete sequence from clone
GSLTSIL42ZC04 of Silique of strain col-0 of Arabidopsis thaliana
AICCGITCITIGATGAACTCAGAGACCAAACGCTCGTTTACCAAATGGACGGCCTCTCC
                                                                                                                                                                                  CGCCTCTCTTCAACTTCAAACAAGAAGTAGCTGGATCATCACCTGAACTGGTCAACAAGT
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Location/Qualifiers
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40.3%; Score 700.8; DB 3;
Best Local Similarity 76.6%; Pred. No. 5.6e-174;
Matches 858; Conservative 0; Mismatches 262;
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Arabidopsis thaliana (thale cress)
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/tissue type="Silique"
/plasmid="pcMVSPORT_6"
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/strain="Col-0"
/db_xref="taxon:3702"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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/clone_lib="Maize Mapping Project/DuPont Cornsensus
                                                                                                                                                                                                                                                                                                                        Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design Overgo Probes Unpublished (2002)
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Pred. No. 1.3e-167;
0; Mismatches 277;
                                                                                                                  mRNA
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/db_xref="MaizeDB:634287"
                                                                                                                AY106255 1745 bp
Zea mays PCO077512 mRNA sequence.
AY106255
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Zea mays
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Matches 843,
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Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G.K.S., Deng, X.W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80488559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 CGAGTTGTAGGAACTGGTTCTTTCGGGATTGTGTTCCAGGCTAAGTGCTTGGAGACGGGG
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                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa (ir
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone lib="Oryza sativa E>
/note="Oryza sativa E>
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Oryza sativa (indica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enharroidaes; Oryzeae; Oryza.
1 (bases 1 to 1197)
Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
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                                                                            Length 1666
                                                                          Score 634; DB 3; Length 16
Pred. No. 2.8e-156;
0; Mismatches 285; Indels
overgo addressing
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
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                                                              CTGCTTCAATACTCTCCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCACATCCGTTC
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                                         GAAAATGCTGTGGATCAGCTCGTGGAAATTATTAAAGGTTCTTGGTACACCAACTCGAGAA
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design (Overgo Probes Unpublished (2002)
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| Da_xref="maizeDB:634655"
| db_xref="taxon:4577"
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Submitted (25-APR-2002) Maize Mapping Project, University of Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA Missouri, Columbia, MO 65211, USA If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.itgr.org, or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
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1 (bases 1 to 1967)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Arthur, L.W., Annafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Unpublished (2002)
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/db_xref="MaizeDB:618897"
/db_xref="taxon:4577"
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/organism="Zea mays"
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An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
further details.
                                                                                                                                                                                                                                                                                          AV821208 689 bp mRNA linear EST 01-APR-2002 AV821208 RAFL2 Arabidopsis thaliana cDNA clone RAFL02-10-D23 5', mRNA sequence. AV821208 GI:19863227
1257 TCATCACCTGAACTGGTCAACAAGTTGATTCCAGACCATATCAAGAGACAATTGGGTCTA 1316
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Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oxono,Y., Sakurai,T., Carninci,P., Kawai,J., Itch,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Large successions of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
Contact: Motoaki Seki
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koydadai, Taukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4959
Fax: 81-298-36-9060
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/note="Site_1: StI; Site_2: XhoI"
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Pred. No. 1.8e-155;
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/dev stage="rosette plants"
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Best Local Similarity 96.5%;
Matches 664; Conservative
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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the covergo addressing of BACs in conjunction with the Maize Mapping Project"
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Pred. No. 1.9e-153;
0; Mismatches 291; Indels 3;
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Best Local Similarity 73.4%;
Matches 811; Conservative
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Craudd, C., Quetler, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
1107 AGGCTGCTTCAATACTCTCCAAGTCTAAGATGCACGCGCTCGAAGCTTGTGCACATCCG 1166
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS91ZE05 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                             1356 CGGCTACTCCAGTACTCCCAAATCTGAGATGCACTGCTATGGAGGCACTTGTTCACCCA
                                                                                                                                               TTCTTTGATGAACTCAGAGAACGCTCGTTTACCAAATGGACGCCTCTCCCCGCCT
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Location/Qualifiers
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/plasmid="pCMVSPORT 6"
/plasmid="pCMVSPORT 6"
/gene="At5g26751"
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/clone="GSLTLS91ZE05"
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/strain="Col-0"
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2 (bases 1 to 1638)
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of CDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/db.xrefe"texacm:3702"
/clone="ApD04f03_f"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/clone_lib="Arabidopsis thaliana above-ground organ two tsix-week old"
six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoIt
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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Submitted (15-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.ibgr.org, or NCBI, www.ncbi.nlm.nih.gov. When the source of the schez CpNA sequences is either Virginia Malbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB:
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
                                                                                                                                                       TCCCTGAGACGTTGTATCGAGTTCTGAAACATTATAGTAGTGCAAACCAAAGAATGCCTC
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051B01AF Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA
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/db_xref="taxon:3702"
/dcv stage==Plant 3 weeks old, three days post infection"
/clone lib="Infected Arabidopsis Leaf"
/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
library of Arabidopsis and B. cichoracearum infected leaf
from three weeks old Arabidopsis plants. Plants were
harvested 3 days after infection and mRNA oligo dT
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dsgaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somerville,S.
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EST sequencing of Erysiphe cichoracearum infected Arabidopsis
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Tel: +45 96358467
Fax: +45 98141808
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    Location/Qualifiers
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/ecotype="Columbia"
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Contact: Karen G. Welinder
Institut for bioteknologi
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTFB37ZG06 of Flowers and buds of strain col-0 of Arabidopsis
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castell V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

Mord IRRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
                        1039 CTGGGCACACCCCACACGTGAAGAAATTAAGTGCATGAATCCAAATTATACCGAGTTTAAA
                                                                                                                                                                               http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
  CTTGGTACACCACTCGAGAAGAATCCGTTGTATGAATCCCAACTACACGATTTCAAG
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/clone="GSLTFB372G06"
/tissue type="Rlowers and bu
/plasmid="pcMvSPORT 6"
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/gene="At1g09840"
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                                                                                                                                                         /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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                                                                          /mol_type="mRNA"
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/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
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Pred. No. 4.8e-145;
0; Mismatches 289;
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                  Location/Qualifiers
                                                        organism="Zea
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www.zmdb.iastate.edu
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 2295)
SMA,L., Wango,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
                                                                                                                                                                                                                                                                                                                                2295 bp DNA linear GSS 21-SEP-2004 OSIFCCO11089 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence. CL964803 GENERAL G
                                    CCTCTCTTCAACTTCAAA---CAAGAAGTAGCTGGATCATCACCTGAACTGGTCAACAAG 1280
                                                               1598 CCACTTTTCAACTTTAAACCGCAAGAGCTATCTGGCATACCTCCTGAAATCGTGAACAGG 1657
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/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"
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Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
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                                                                                                                                                                                                                                                                                                                                                                                                           GCGGAGCGAGTTGTTGGTACAGGCTCGTTCGGGCATCGTTTTCCAAGCAAAATGTTTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 TCAGAACATGTTGTTGGTACTGGTTCCTTTGGCATGGTTTTCCAAGCTAAATGTAGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAACTCTACACCTATCAGATTTGCAGGGGGCTTGCTTACATCCATAATTCCTTTGGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                564 TIGIAICGAGTICTGAAACATTAIAGTAGTGCAAACCAAAGAAIGCCICTTGTCTAIGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACTITACAGITATCAGATCTTCCGGGGACTTGCTTACATTCACAGITGCCCGGGAGTT
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                                                                                                                                                                                                                               GATGATGAGAGATAGTGAACCAGATATTATTGATGGGGCTGGTGATGAGCCTGGTCAT
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                                                                                                                  ë.
                                                               Length 1870;
                                                                                                               Indels
                                                         Score 585.4; DB 3;
Pred. No. 2.1e-143;
0; Mismatches 306;
                                                      Query Match
33.7%;
Best Local Similarity 71.7%;
Matches 782; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1058
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// Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse at University of California, Riverside. The scion was a open-pollinate of Very probably selfed)
seedling of Poncirus trifoliata cv Pomeroy that was selected as homozygous for the Ctv resistance gene. The roctstock was sweet orange infected with citrus tristera virus (CTV) isolate T514 over 1 year before sampling (CTV infects sweet orange, but not genotypes carrying the Ctv resistance gene. Shoots 10-30 cm long were harvested in October 2000, and the green phicoem (bark) was removed and frozen quickly in dry ice. Total RNA was extracted using Trizol reagent (Gibco). Poly(A) RNA was purified, a cDNA library was made, and 0.5 million primary lambda cDNA clones were in vivo excised to give a population of pellors were in vivo excised to give a population of performed in the ML Roose lab at the University of California Riverside by X. Ye. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the University of California Riverside Genomics Institute, Chromatogram files were transmitted to UC Riverside (by Chromatogram files were transmitted (by Wanamsker) using the Harv&ST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 gecceacearaaceacarererecrecrerrerrerreaceseareacearereacea 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 AACTGGGGAGACTGTGGCTATCAAGAAGGTTTTGCAGGACAGAAGATATAAAGAATGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATTATTTCCACCACAATCGGTGGCAAAAATGGTGAACCAAAACAGACAATTAGTTACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383 GACTGGAGAAACCGTGGCGATAAAGAAGGTTTTGCAAGATAGAAGATACAAGAACCGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 GTTGTATCGAGTTCTGAAACATTATAGTAGTGCAAAACAAAGAATGCCTCTTGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                     /db_xref="taxon:37690"
/clone="UCRPT01 06_F05"
/tissue_type="Phloem"
/dav_stage="10 - 30 as shoots"
/lab_host="E. coli TJC121"
/clone_lib="Poncirus trifoliata CTV-challenged cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 887;
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                                                                                                                                                                                                                                                - UCR"
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1 (Sparantophyta, Magnoliophyta, eudicotyledons, core eudicots, 10 (Sparantophyta, Pederici, C.F., Close, T.J., Fenton, R.D., Manamaker, S., Choi, Y. and Kingan, T. Development of EST Resources and New Genetic Markers for California Citrus - Poncirus trifoliata CTV-challenged phloem - UCR Unpublished (2003)

Contact: Mikeal Roose
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UCRPT01_06_F05_T3 Poncirus trifoliata CTV-challenged cDNA library - UCR Poncirus trifoliata cDNA clone UCRPT01_06_F05, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          983 TCGAGAAGAAATCCGTTGTATGAATCCCAACTACACAGATTTCAAGTTCCCACAGATAAA 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1043 GGCCCATCCCTGGCACAAGATCTTCCACAAAGGATGCCCCCAGAAGCGGTTGATTTGGC 1102
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396 CTCTACCACAAGCAGAGATGAACTTTTCCTTAACTTAGTCATGGAGTTTCTTCCCGAGTC 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTGATATCTGGTCTGCTTGTGTTCTTGCTGAGCTTCTTGGTCAGCCATTATT 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCGGAGAAATGCTGTGGATCAGCTCGTGGAAATTATTAAAGTTCTTGGTACACCAAC 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              816 TCCTGGTGAAAGTGCAGTGGACCAGCTTGTTGAGATAATTAAGGTTTTGGGTACTACCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            936 AGCATGCCCATGGCACAAGATCTTCCACAAGCGAATGTCTCCCGAAGCAATAGATCTTGT 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sciences, University of California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     636 GGTCTGTGATTTTGGGAGTGCTAAAATGCTGATTAAAGGTGAAGCAAATATATCTTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  743 AATCTGTGACTTTGGCAGTGCGAAACAGCTCGTTAAAGGTGAACCAAACATTTCTTACAT
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                                                                                                                                                     456 ACTITATCGIGICCICAAACACIACAAAGAIAIGAAGCAGGAGGAIGCCACTIAIAIAIT
                                                                                                                                                                                                                                                                          516 CAAACTITACATGIATCAGATATTCCGCGGATTAGCTTACATTCACACTGTTCCTAGAGT
                                                                                                                                                                                                                                                                                                                                         TTGTCACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCTCTTACTCATCAAGTCAA
                                                                                               GTTGTATCGAGTTCTGAAACATTATAGTAGTGCAAACCAAAGAATGCCTCTTGTCTATGT
                                                                                                                                                                                                                    TAAACTITACAGTIATCAGATCTICCGGGGACTTGCTTACATTCACAGTTGCCCGGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              996 GTCCCGTCTCCTTCAGTATTCGCCAAATCTGCGATGTACTGCG 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1103 ATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCACAGCG 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Botany & Plant Sc
Riverside, CA, 92521-0124, USA
Tel: 9097874137
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Location/Qualifiers
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/clone libe potential abiotic stress cDNA library"
/note="Vector: pCMVSport6.1; Site 1: EcoR1; Site 2: Not1;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
thous separate sets of plants. Set I involved saturation of
thous not library work and tissues were harvested at
following application of the salt stress (leaves: 2hr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             924 bp mRNA linear EST 03-AUG-2004 stress cDNA library Solanum tuberosum cDNA
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1 (bases 1 to 934)

1 (bases 1 to 934)

1 elell C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from abiotic stressed potato tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robin Buell
The Institute for Genomic Research
3712 Medical Center Dr. Rockville, MD 20850, USA
Bmail: potato-arrayelyr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
CATGTATAGAGTTTTGAAGCATTACAGCAGTGCAAATCAGAGAATGCCCCCTCATATAGTGT
                                                                                                                                                                                                                            542 ridecaradedariricaaccicaaaaccirridericarccicriacrecaecraa
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                                                                           TAAACTTTACAGTTATCAGATCTTCCGGGGACTTGCTTACATTCACAGTTGCCCGGGAGT
                                                                                                       482 GAAACTITATACGTACGTACGAGATTITCAGGGGCCTGGCTTACATCCACACTGTTCCTCGAGT
                                                                                                                                                                             TIGICACAGAGAICTAAAGCCTCAAAATCTICTGGTTGATCCTCTTACTCATCAAGTCAA
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/mol_type="mRNA"
/cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST712488 potato abiotic stress cDNA clone POAC457 5' end, mRNA sequence.
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/clone="POAC457"
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6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were near stressed at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RAM was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the CDNA library. RNA sample."

61 AGAAGGTTTTACAGGACAAGCGGTATAAAAACCGTGAACTACAACTGATGCGCTTGATGG 120 1 GGTCCTTTGGGATAGTGTTTCAGGCAAATGCTTGGAAACTGGAGAGACTGTGGCCATAA AGAAGGTTTTGCAAGATAGAAGATACAAGAACCGAGAACTTCAGTTGATGCGTGTGTGG Gaps GCTCGTTCGGGATCGTTTTCCAAGCAAATGTTTGGAGACTGGAGAAACCGTGGCGATAA **ATCATCCGAATGTGGTTTGTTTGAAGCATTGCTTTTTTCGACTACAGAGAAGACGAGC** ö 7; Length 924; IndelB tch 33.4%; Score 579.8; DB 7; al Similarity 76.9%; Pred. No. 5.5e-142; 707; Conservative 0; Mismatches 212; Query Match Best Local Si Matches 707, 346 406 121 466 526 셤 ò 셤 g ò ò ò

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Copyright (c) 1993 - 2005 Compugen Ltd.
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SUMMARIES

	Description	X94938 A.thaliana	AY094423 Arabidops	AY064020 Arabidops	AY087542 Arabidops	AY096698 Arabidops	AF019927 Arabidops	AY035048 Arabidops	X99696 A.thaliana	AY051053 Arabidops	X94939 A.thaliana	AY086529 Arabidops	AY075699 Arabidops	CQ804868 Sequence	AX506180 Sequence	AK073725 Oryza sat	AK100950 Oryza sat	AK102147 Oryza sat	AK105665 Oryza sat	BT009253 Triticum
	ID	ATASKDZET	AY094423	AY064020	AY087542	AY096698	AF019927	AY035048	ATASKIOTA	AY051053	ATASKRNA	AY086529	AY075699	CQ804868	AX506180	AK073725	AK100950	AK102147	AK105665	BT009253
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æ	Query Match	100.0	94.5	94.0	90.3	77.2	59.6	59.5	59.4	57.4	44.9	44.8	44.7	44.7	44.7	42.4	40.5	40.5	40.4	40.4
	Score	1636	1546.4	1537.8	1478	1263.6	975.6	974.2	972.2	939.8	734.6	733	731.4	730.8	730.8	694	662.8	662.8	661.2	660.4
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Y13437 Oryza gativ	BT010466 Arabidops	AY065043 Arabidops	X83619 P.hybrida m	AY339067 Physcomit	AY142595 Arabidops	AF428327 Arabidops	AY046024 Arabidops	X77763 N.tabacum N	X68525 A.thaliana	X75432 A.thaliana	X68411 A.medicago	AY085752 Arabidops	Y08607 N.tabacum m	X75431 A.thaliana	AX507663 Sequence	AY093347 Arabidops	AY062713 Arabidops	AB059621 Oryza sat	AK099742 Oryza sat	AJ224163 Nicotiana	AK104687 Oryza sat	AK068737 Oryza sat	AK072390 Oryza sat	AY339066 Physcomit	X68410 A.medicago	
OSKETHA	BT010466	AY065043	PHPSK4	AY339067	AY142595	AF428327	AY046024	NTNTK1RN	ATASKA	ATRNAASKA	AMMSK1A	AY085752	NTNSK6	ATRNAASKG	AX507663	AY093347	AY062713	AB059621	AK099742 ·	NTAJ4163	AK104687	AK068737	AK072390	AY339066	AMMSK2A	
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40.3	37.7	37.7	37.3	37.0	36.8	36.8	36.8	36.6	36.3	36.3	36.3	36.1	36.0	35.9	35.9	35.9	35.9	35.7	35.6	35.6	35.5	35.5	35.5	35.4	35.1	
659.6	616.6	616.6	609.8	605.2	602.2	602.2	602.2	599	594.2	594.2	593.6	591	588.4	588	587.8	587.8	587.8	584.2	582.6	581.8	581	581	580.6	579.2	573.8	
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

ATASKDZET 1636 bp mRNA linear PLN 13-FEB-1998 A.thaliana mRNA for shaggy-like kinase dzeta. X94938 X94938.1 GI:1161509 ASK dzeta gene; serine/threonine kinase; shaggy-like kinase dzeta. Arabidopsis thaliana (thale cress)	Arabidopsis Inaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 1 Arais M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and	Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99569) (PRR97-008)	Plant Physiol. 113, 306-306 (1997)  2 (bases 1 to 1636) Dornelas,M.C. Direct Submission Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de París-Sud, Institut de Biotechnologie des Plantes, Centre de Recherches sur les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405		1. 1636 /gene="ASK dzeta" 45. 1283 /gene="ASK dzeta" /codon_start=1 /product="shaggy-like kinase dzeta"
RESULT 1 ATASKDZET LOCUS DEPINITION ACCESSION VERSION KEYWORDS SOURCE	ORGANISM REFERENCE AUTHORS	TITLE	JOURNAL REFERENCE AUTHORS TITLE JOURNAL	COMMENT FEATURES SOURCE	GDS

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CTCCTGTATCAGTATTTGTATATGTTTTTGTCCTTGAAATGAAACAAAATCGATTCCAAA 1560
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FLI CDNA.
Axabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots,
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/db_xref="UniProt/Swiss-Prot:039010"
/translation="Wisis PLOPPOPPELAPOPPHLHGGDSLKRRPDIDNDKEMSAAVI
EGNDAYTGHIISTIGGKNGEPKOTISYMARRVOGTGSFGIVFQAKCLETGSSVAIKK
VLQDRRYKNRELQLMRLMDHPNVVSLKHGFFSTTRDBLFLNUMEYVPETLYRVLKH
YTSSNORMPIFYVKLYYYOIRGLAYIHTAPGVCHRDIRFONLLVDPHTHQCKLCDFG
SAKVLVKGEPNISYICSRYYRAPELIFGATEYTSSIDIWSAGCVLAELLGQPLFPGE
RLLQYSPSLRCTALEAAAHPFNELERGNNPYTDFRRPQIRAHFWRHKWPPBAIDLAS
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Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J.,
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Chang, B., Dale, J.M., Goldsmith, A.D.,
Hayashizaki, Y., Lam, B., Led, J.M., Lin, J., Miranda, M., Narusaka, M.,
Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T.,
Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,
Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
Theologis, A. and Ecker, J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                            collection and clustering of RAFL cDNAS (RAFL cDNA: 'RIKEN Arbidopals Rull-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kawiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J. Bowser, L., Chang, E., Dale, J. M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
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Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayasahizaki, Y., Ishida, J., Jones, T., Kaniya, A., Karlin-Neumann, G., Kawai, J., Lam, B. Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, L.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Theologis, A. and Ecker, J.R.
Arabidopsis cDNA clones
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Location/Qualifiers
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    organism="Arabidopsis thaliana"

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Pred. No. 5.9e-278;
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/clone="RAFL05-02-L16(R21926)"
/ecotype="Columbia"
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/db_xref="taxon:3702"
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Best Local Similarity 99.6
Matches 1550; Conservative
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                                                                                                                                                              REFERENCE
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CTTTGAAACGTCGTCCCGATATAGACAACGACAAGGAAATGTCTGCTGCTGTTATAGAAG
                                                                                                                                    GAAATGATGCTGTTACCGGTCACATAATTTCTACTACAATTGGAGGCAAAAATGGTGAAC
                                                                                                                                                      GAAATGATGCTGTTACCGGTCACATAATTTCTACTACAATTGGAGGCAAAAATGGTGAAC
                                                                                                                                                                                                            CTAAACAGACCATTAGTTACATGGCCGAACGTGTTGTTGGAACAGGATCATTCGGAATTG
                                                                                                                                                                                                                                                                                         TATTCCAGGCAAAATGCTTGGAAACTGGAGAATCAGTAGCCATTAAGAAGGTTTTGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       636 ATATCCATACTGCTCCTGGTGTGTGCCACAGAGATGTGAAACCACAAAATCTTTTGGTTG
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Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Mairanda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
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                                                                                                                                                                                         Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
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Location/Qualifiers
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Pred. No. 2.3e-276;
0; Mismatches 7; Indels
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(Lambda ZAP) as a XhoI/SstI insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                              thaliana"
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1293. .1566
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Best Local Similarity 99.5%;
Matches 1542; Conservative
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1566)
Samada, K., Luu, S. K., Sakano, H., Pham, P. K., Banh, J., Chung, M. K., Goldsmith, A. D., Lee, J. M., Quach, H. L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Karlin, Pkeumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J. R. and Theologis, A. Banno, F., Chang, E., Dale, J. M., Goldsmith, A. D., Samada, K., Banh, J., Banno, F., Chang, E., Dale, J. M., Goldsmith, A. D., Cheuk, R., Hayashizaki, Y., Shinday, J., Carninci, P., Chen, H., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Shinnozaki, K., Davis, R.W., Seki, M., Narusaka, M., Narusaka, M., Narusaka, M., Narusaka, M., Seki, M., Shinn, P., Southwick, A., Shinnozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Bhinnozaki, K., Davis, R.W., Becker, J.R. and Theologis, A. Bhinnozaki, K., Davis, R.W., Becker, J.R. and Theologis, A. Bhinnozaki, K., Davis, R.W., Becker, J.R. and Theologis, A. Bhinnozaki, K., Davis, R.W., Becker, J.R. and Theologis, A. Bhinnozaki, R. Davis, R.W., Becker, J.R. and Theologis, A. Bhinnozaki, M. Davis, R.W., Berker, J.R. and Theologis, A. Bhinnozaki, M. Davis, R.W., Berker, J.R. and Theologis, A. Bhinnozaki, M. Davis, R.W., R.W.
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                                                                                                                                                                                                                                                       AY064020 1566 bp mRNA linear PLN 18-SEP-2002 Arabidopsis thaliana putative shaggy protein kinase dzeta (At2g30980) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                   CGCCTTATGGAATGAAGGAGAGGGAGATTTACTTCTCTCTGATTAACTAAGTATCAGCTT 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAGAAGAGATGATGTCTCCTCCTTAGACGTGGCCAATTCAGCTTTTTGAGAAATCAGG 1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (19-NOV-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA Ricet, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA: RIKEN Arabidopsis Full-Length CDNA: Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J., Banno,F., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M.,
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                                       1176 TICCAAATGGCCGACCTCTACCACCGTTGTTCAACTTCAAACAAGAGTTGTCTGGGGGCTT
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VERSION
KEYWORDS
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Direct Submitted (11-MRR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the considered to be 5'-truncated if it lacks the sequence is considered to be 3'-truncated if it lacks the general polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequences from Col-0. Genset carried out the library production and sequences from fine it location of clones, and sequence assembly. /translation="MYSIPLGPPQPPSLAPQPPHLHGGDSLKRRPDIDNDKEMSAAVI EGNDAVTGHIISTTIGGKNGEPKQTISYMAERVVGTGSFGIVFQAKCLETGESVAIKK VLODRRYKNRELQLMRLMDHPNVOSLHGFPSTTRRBLFLALLWMEYVPETLYRVLKH YTGSNQRMPIPYKLYTYGIPGLAY HTAPGVCHRDVKPQNLLVDPLTHQCKLCDFG SAKVLVNGRANISYTCSRYYRSPELIFGAFEYTSSIDIMSAGCVLABELLIGOPLFPGE NSVDRLVEIIKVLGTPTREBIRCMNPYTDFRFPQIKAHPWHKVFHKRMPPEAIDLAS RLLQYSPSLRCTALEACAHPFFNELREPNARLPNGRPLPPLFNGE 1450 AGGCGATGATTGTGTCCTATTATATTCTTTTGTTCACTGACTTGTAGAGAGATACTTTT 1509 PLN 14-APR-2003 Eukaryophyta; Iracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Full-Length cDNA from Arabidopsis thaliana Unpublished 3 (bases 1 to 1503) Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and (bases 1 to 1503) rover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome /codon\_start=1 /product="putative shaggy-like protein kinase dzeta" /protein\_id="AAM65084.1" /db\_xref="G1:21593132" 1503 bp mRNA linear PLN i Arabidopsis thaliana clone 36479 mRNA, complete sequence. AY087542. AY087542.1 GI:21406280 1510 CTCCTGTATCAGTATTTGTATATTTTTTTTTTGTCCTTGAAATGAAAAAAA 1558

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LOCUS AF019927
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YTSSNQRMPIFYKLYTYYOIPRGLIFGATETTSSIDIWSAGCVTLAELLHGQPLEDFG
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SAKVLVKGERNISYTCSRYYRAPELIFGATETTSSIDIWSAGVTLAELLHGQPLEPGE
SAKVLVKGERNISYTCSRYRAPREIREFRAMPHRUPREPREPGE
RLLQYSPSIRCTALEACAHPFNELREPNARLPNGRPLPPLFNFKQELSGASPELINR
LIPPEHVRRQWNGGFPFQAGF"
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Location/Qualifiers
       Ishida,J.,
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                                                                                              The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORP) clones using the RAFL cDNAs: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E. Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Chriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H. Cheuk,R., Jones,T., Karlin-Neumann,G., Kin,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
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Arabidopsis Full-Length cDNA'): Seki.M., Narusaka,M., Ish
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J.,
Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                              Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (/PGEC) contributed equally to this work as PIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.2%; Score 1263.6; DB 8; Length 1270;
larity 99.7%; Pred. No. 2.5e-225;
Conservative 0; Mismatches 4; Indels 0;
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/mol_type="mRNA"
/db_xref="taxon:3702"
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                                                                                              TGAAGCACTATACTAGTTCAAACCAGCGGATGCCTATCTTCTATGTCAAACTTTACACAT
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  TAGCCATTAAGAAGGTTTTGCAAGATCGCCGTTATAAAAACCGAGAGTTGCAATTAATGC
                                                                                                                                                                             GAGATGAGCTCTTCCTCAACCTTGTTATGGAGTATGTACCTGAGACTTTATATACGGGTTT
                                                                                                                                                                                                                                                      TAAAACCACAAAATCTTTTGGTTGATCCCCACACCCATCAGTGTAAGCTCTGTGATTTTG
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                                                                          CTTCTCTACAACGACTA
                                                                                                                                                       GAGATGAGCTCTTCCTCAATCTCGTTATGGAGTATGTACCAGAGACATTGTACCGGGTTT
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                                                                          GACTAATGGACCATCCAAATGTGGTTTCCTTGAAGCATTGTTT
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/codon_start=1
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SSNQRMPIFYVKLYYYQIFRGLAYIHTVPGYCHRDVKRDVLNDPLTHQVKLCDFGSA
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VOOLWEIIKTGTPTREEIRCKNPNYTDFRFPOIKAHPWHKVFHKRNPPEAIDLASRL
LOYSPSLRCTALEACAHPFFNELREPNARLPNGRPLPPLFNFKGELGGASMELINRLI
PEHVRROMSYGLQON
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Piao,H.L., Pih,K.T., Lim,J.H., Kang,S.G., Jin,J.B., Kim,S.H. and
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                                                                                                                                                                                                                                                                                                                                                                                                         and Biotechnology
Chinju 660-701,
                                                                                                                                                                                                                           An Arabidopsis GSK3/shaggy-like gene that complements yeast salt stress-sensitive mutants is induced by NaCl and abscisic acid Plant Physiol. 119 (4), 1527-1534 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGGAACAGGTTCATTCGGGATTGTTTTTCAGGCGAAATGCTTGGAAACTGGAAAACTGGAAATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAATTGGAGGCAAAATGGTGAACCTAAACAGACCATTAGTTACATGGCCGAACGTGTTG
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                                                                                                                                                                                                                                                                                                                                                Jin, J.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mgkNA"

/mol_type="mgkNA"

fatrain="Columbia"

/db_xref="taxon:3702"

1. 1552

1. 1552

/gene="GSK1"

/note="complements the yeast calcineurin mutation"

26. .1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1572;
                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1572)
Piao,H.L., Jang,H.J., Pih,K.T., Lim,J.H., Kang,S.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                     Hwang,I.
Direct Submission
Submitted (18-AUG-1997) Plant Molecular Biology a
Research Center, Gyeongsang National University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 975.6; DB 8;
Pred. No. 9.8e-172;
0; Mismatches 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .1572
/organism="Arabidopsis thaliana"
                                                                          Arabidopsis thaliana (thale cress)
complete cds.
AF019927
AF019927.1 GI:2444276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 77.3%;
Matches 1221; Conservative
                                                                                            Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                        SOURCE
ORGANISM
                ACCESSION
VERSION
KEYWORDS
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PUBMED
REFERENCE
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JOURNAL
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                                                                                                                                                                       REFERENCE
                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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/tränslation="MASLPLGPQPHALAPPLQLHDGDALKRRPELDSDKEMSAAVIEG
NDAVTGHIISTTIGGKNGEPKQTISYMAERVVGTGSFGIVFQAKCLETGESVAIKKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDRRYKKKRELQLMRPMDHPNVĪSLKHCFFSTTSRDELFLNLVMEYVPETLYRVLRHYT
SSNQRMPIFYVKLYTYQIFRGLAYIHTVPGVCHRDVKPQNLLVDPLTHQVKLCDFGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVLVKGEPNISYICSRYYRAPELIFGATEYTASIDIWSAGCVLAELLLGQPLFPGENS
VDQLVEIIKVLGTPTREEIRCMNPNYTDFRFPQIKAHPWHKVFHKRMPPEAIDLASRL
LQYSPSLRCTALEACAHPFFNELREPNARLPNGRPLPPLFNFKQELGGASMELINRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTCGTCCCGATATAGACAACGACAAGGAAATGTCTGCTGCTGTTATAGAAGGAAATGAT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCGTCCTGAATTGGATTCTGATAAGGAAATGTCTGCAGCTGTTATTGAGGGAAATGAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGTTACCGGTCACATAATTTCTACTACAATTGGAGGCAAAAATGGTGAACCTAAAACAG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 gcgaaariccrregaaacregagaarcagragccarraaaaaggrerregaagarcaacc 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCAGCCTCCGTCTTTAGCTCCTCAGCCGCCGCATCTTCACGCGGGGGAGATTCTTTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 ACCATTAGTTACATGGCTGAGCGGGTTGTTGGAACAGGTTCATTCGGGATTGTTTTCAG
                                                                                                                                                                          'note="This clone is in a modified pBluescript vector [FLC-1] as a BamH/XhoI insert."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAAAATGCTTGGAAAACTGGAGAATCAGTAGCCATTAAGAAGGTTTTGCAAGATCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATAAAAACCGAGAGTTGCAATTAATGCGACTAATGGACCATCCAAATGTGGTTTCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                 note="contains an eukaryotic protein kinase PF|00069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCAGTGAGAGAGAGGTTAGAGCTGTAAAAAGCACATGACTTCGATACCATTGGGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="At1g06390"
/note="not present in genomic sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 974.2; DB 8;
Pred. No. 1.8e-171;
0; Mismatches 333;
      organism="Arabidopsis thaliana"
                                                                                           'chromosome="1"
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/protein_id="AAK59553.1"
/db_xref="GI:14334750"
                                                         db xref="taxon:3702"
                                                                                                                                                  ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="compared to
                                                                                                                                                                                                                                                                                                                                                                                         gene="At1g06390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1441. .1442
/gene="At1g06390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="At1g06390"
                                                                                                                                                                                                                                                                        gene="At1g06390"
                                                                                                                                                                                                                                                                                                                               gene="At1g06390"
                                 type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEHVRRQMSTGLQNS"
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1567
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Best Local Similarity 77.5%;
Matches 1241; Conservative 0
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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E (Dases 1 to 1582)

S Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldenith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Jones, T., Kamiya, A., Karlını-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Scki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
AY035048 116-2002 mRNA linear PLN 18-SEP-2002
Arabidopsis thaliana putative shaggy kinase (At1g06390) mRNA,
                                                                                                                                                                                                                                                                  1493 AAACAATTCTGACAGATACGTAGAGACAAAAGAAAACGAGGTGATAATATTAAACCAAA 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-MAY-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94110, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA: RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1582)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G.
Bowser,L., Carninci,P., Chen,H., Cheuk,R., Haysshizaki,Y.,
Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
Kim,C., Kosesma, E., Lam,B., Lin,J., Meyers,M.C., Miranda,M.,
Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                           ACTGACTTGTAGAGAGATACTTTTCTCCTGTATCAGTATTTGTATATGTTTTTGTCCTTG
                                                                                                                                                                                                                                                                                                                                                                                      1553 AAAAAAAAAAAAAAAAA 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AY035048.1 GI:14334749
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL REFERENCE AUTHORS

DEFINITION

RESULT 7 AY035048 LOCUS

ACCESSION

4

Gaps

27;

Length 1582; Indels 128 121

TITLE JOURNAL

COMMENT

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429 AAGCATTGTTTCTTCTACAACGACTAGAGATGAGCTCTTCCTCAATCTCGTTATGGAG 488

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Harea New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008)

Plant Physiol. 113, 306-306 (1997)

2 (bases 1 to 1614)

Dornelas, M.C.
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Submitted (01-AUG-1996) M.C. Dornelas, Universite De Paris-Sud
(Parisxi), Institut De Biotechnologie Des Plantes, Lab. Biol. Du
Developpement Des Plantes, Batiment 630, F-91405 Orsay Cedex,
FRANCE
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A.thaliana mRNa for shaggy-like kinase iota.
X99696
                                                                                                                                                                       Query Match 59.4%; Score 972.2; DB 8; Best Local Similarity 77.0%; Pred. No. 4.2e-171; Matches 1234; Conservative 0; Mismatches 343;
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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E 1 (bases 1 to 1255)

S Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,P.,
Lee,J.M., Toriumi,M., Yu,G., Brooke,S., Chao,Q., Chen,H.,
Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M.,
Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and AY051053 1255 bp mRNA linear PLN 18-SEP-2002 Arabidopsis thaliana putative shaggy kinase (At1g06390) mRNA, complete cds. ATCAGCTTCTATACCCGTAGTAAAGTCATATTCAGCTTTTTGAGAAATCAGATGCTGATA 1451 1512 TGTATTTTTGTATATGTTTTTGTCTGTAAAACAATTCTGACAGATACGTAGAGACAAAAG 1571 Submitted (02-AUG-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA.

The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Pull-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satu,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K. The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Yamada, K. Liu, S. X., Pham, P. K., Banh, J., Banno, F., Dale, J. M., Yamada, K., Liu, S. X., Pham, P. K., Banh, J., Banno, F., Dale, J. M., Jodosan, K., Liu, S. X., Lee, J. M., Ondocra, C. Sowaer, L., Tang, C. C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurah, T., Sakurah, T., Sakurah, T., Sakurah, T., Sakurah, T., Sakurah, T., Sakurah, S. Shinn, P., Southwick, A., Tracy, S. E., Shinozaki, K., Davis, R. W., Ecker, J. R. e. -----recarereterasasasasasas GGAATGAAGGAGAGAGATTTACTTCTCTCTGATTAACTAAGTATCAGCTTCTGAGAAG CAGGITTACTACTATTATTTGATAGTTGACAGGTTCAACAGTATATTAACCACGACTATT AGATGATGTCTCCTCTTAGACGTGGCCAATTCAGCTTTTTGAGAAATCAGGAGGCGATG ATTIGTICCCATTATAATCTTTTTGTTCACTGACTTGTAGAGAGATACTTTTCTCCTGTA

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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008)
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A.thaliana mRNA for shaggy-like kinase etha.
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                                                                                                                                   Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers
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                                                                        d equally (SSP
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Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koseema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tracy, S.E., Davis, R.W., Ecker, J.R. and Theologis, A.
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                                                                         Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (/PGEC) contributed equally to this work as PIs.
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87.3%; Pred. No. 4.5e-165;
iive 0; Mismatches 149;
                                                                                                                                                                                             /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
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/note="This clone is in
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Arabidopsis thaliana clone 256076 mRNA, complete sequence.
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FLI CDNA.
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Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
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/db xref="G1:1161512"
/db xref="G1:1161512"
/db xref="G0A:039011"
/db xref="G0A:039011"
/db xref="mibrot/swise-prot:039011"
/db xref="mibrot/swise-prot:03901
                                       Dornelas, M.C.
Direct Submission
Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud,
Institut de Biotechnologie des Plantes, Centre de Recherches sur
les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405
ORSAY Cedex, FRANCE
Corresponding genomic sequence is found in Y08947.
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                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="Columbia ecotype"
/db_xref="taxon:3702"
/tissue type="mix of several tissue typecans and developmental stages"
/clone lib="Newman's lambda Zip Lox"
/dev_stage="young shoots"
1. 1738
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/organism≂"Arabidopsis thaliana"
nt Physiol. 113, 306-306 (1997)
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Tolassis; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1670)
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D.,
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                                                                                                                                                                                                                                                                                                                                  Direct Submission

Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5-truncated; less than one percent are 3-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the cereminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Lack copyes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequences from Col-0. Genset carried out the library production and sequenceing of the location/Qualifiers
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vvgtgsfgivfqakcletgetvaikkvlqdrryknrelqlmrvmdhpnvvclkhcffs
ttskdelflnlvmeyvpesllyrvlkhyssanqrmplvyvklymyqifrglayihnvag
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FPQIKAHPWHKIFHKRMPPERIDFASRLLQYSPSLRCTALEACAHPFFDELREPNARL
PNGRPPPPLENFKQEYAGSSPBLVNKLIPDHIKRQLGISFLNQSGT"
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Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R.
Feldmann, K.
                                Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R.
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/db_xref="GI:21554512"
Brover, V., Troukhan, M., Alexandrov, N., Lu, Feldmann, K.
Full-Length cDNA from Arabidopsis thaliana
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TTSIDIWSAGCVLAELLLGQPLFPGBRNAVDQLVEIIKVLGTPTREEIRCMNPHTTDFR
PPQIKAHPWHKIFHKRMPPEAIDFASRLLQYSPSLRCTALEACAHPFFDEHRBPNARL
                                                                                                                                                                                                                                                                                                                                                        Submitted (25-JAN-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                        collection and clustering of RAFL CDNAS (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., and Shinozaki,K.
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                                                                                                                                                            2. (bases 1 to 1670)
Shinn, P., Chenk, R., Kim, C.J., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D.,
Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M.,
Nguyen, M., Seki, M., Sulm, C.J., Quach, H.L., Sakurai, T.,
Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,
Tamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers
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               Karlin-Neumann, G.,
Narusaka, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J. Bowser, L., Chang, E., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Foriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A.,
Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satcou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Theologis,A. and Ecker,J.R.
Arabidopsis cDNA clones
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/note="shaggy-like protein kinase
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Matches 888; Conservative
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use patent: WO 0216655-A 875 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG (CH)
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ATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGCCACAGAGTATACATCA
                                                                                                                           TTCCCGGGAGAAATTCTCTGGACCAGCTAGTGGGAATCATAAAGGTTCTTGGTACTCCA
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                  601 ATCTGCTCACGATTCTACCGTGCACCCCGAGCTCATATTTGGTGCCACTGAGTACACACT
                                                                                                                                                 TCCATTGATATATGGTCTGCTGGTTGTGTTCTGGCAGAGCTACTTCTTGGGCAGCGTTA
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Sequence 875 from Patent W00216655.
AX506180.1 GI:23387417
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheol
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                    Inze,D., de Veylder,L. and Vlieghe,K.
Identification of novel e2f target genes and use thereof
Patent: WO 2004035798-A 1279 29-APR-2004;
CropDesign N.V. (BE)
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Pred. No. 3.6e-126;
0; Mismatches 257;
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db xref="taxon:3702"
                                                                                                            CQ804868 1143 bp DNA
Sequence 1279 from Patent WO2004035798.
CQ804868. GI:47111068
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Best Local Similarity 77.5%;
Matches 885; Conservative
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, W., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Li, C., Ohtsuki, K., Shihiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narkawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Kusumegi, T., Kodama, T., Wantano, K., Yokomizo, S., Niikura, J., Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Kanodo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y., Scollection, mapping, and annotation of over 28,000 cDNA clones from
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                                                                                                                                                                                                                                      2055 bp mRNA linear PLN 24-JUL-2003 oryza sativa (japonica cultivar-group) cDNA clone:J033061L20, full AK073725
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:eKhchlemias.affrc.go.jp,
Tel:129-838-7007, Fax:81-22-838-7007, Fax:81-22-838-7007, Fax:81-22-888-7007, Fax:81-22-888-7007, Fax:81-22-888-7007, Fax:81-22-888-7007, Fax:81-22-888-7007, Fax:81-22-888-7007, Fax:81-20-888-7007, Fax:81-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnolitophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza,
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Addimura, T. Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kucsaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Kodama, T., Kucsaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Sugiyama, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanadawa, S., Karch, H., Kouda, M., Kajawa, I., Kanagawa, S., Karch, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Oato, N., Sasaki, D., Sato, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Shiraki, T., Sogabe, Y., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Tayakashi, F., Takaku-Akahira, S., Tanaka, Y., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Obneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
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Matches 856; Conserv
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                815 AAAAATGTTGGTTAAAGGTGAAGCAAACATATCGTATATATGTTCACGTTATTACCGTGC
                                                                                                              824 TTGTGTTCTGGCAGAGCTACTTCTTGGGCAGCCGTTATTCCCGGGAGAAATTCTGTGGA
                                                                                                                                                                                                                                                       1055 GAÁTCCCAACTACACAGAATTCAGATTTCCTCAGATTAAAGCTCACCCATGGCACAAGAT
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                                                        TCCAGAACTCATCTTTGGTGCCACAGAGTATACATCATCCATTGATATAGGTCTGCTGG
                                                                        935 GIGTGTTCTTGCTGAGTTGCTCCTTGGCCAGCCTCTTTCCTGGTGAAAGTGCAGTGGA
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Search completed: June 23, 2005, 21:28:27 Job time: 11446.2 secs

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RESULT 1
                                                                                        June 23, 2005, 03:29:55; Search time 1283.09 Seconds (without alignments) 7547.973 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aac47511 Arabidops Aac47511 Arabidops Aac54073 Arabidops Aac7997 Arabidops Aal54221 cDNA of w Aac47206 Arabidops Abz13070 Arabidops Adn73384 Thale cre Aac41916 Arabidops Adn73384 Thale cre Aac41916 Arabidops Adn73384 Thale cre Aac48114 Eam mays Acc57973 Soybean p Aac48014 Zea mays Aac48014 Zea mays Aac47014 Wheat gly Aac51694 Zea mays Aac47761 Zea mays Aac47761 Zea mays Aac47761 Zea mays Aac47761 Zea mays Aac47762 Zea mays Aac47762 Zea mays
SUMMARIES B ID	3 AAC47571 3 AAC47571 3 AAC47975 3 AAC47997 10 AAL54221 3 AAC47206 6 ABZ13070 6 ABZ13070 8 ACC57970 8 ACC57970 8 ACC57970 8 ACC57970 8 ACC57973 3 AAC47761 3 AAC47763 3 AAC47763
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* Query Match Length DB	0.000000000000000000000000000000000000
Score	1484 1984 1984 1984 1986 1986 1986 1986 1986 1986 1986 1986
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AAC46604	ABZ14553	AAC45767	ADQ37156	ADQ15740	ACC57977	AAH47001	ABQ82531	AAC43095	ADN72934	AAC42818	AAL55586	ACC57974	AAH47003	ABQ82533	ACC57969	ACC57971	ABZ12869	ADG87959	ADN73136	ACC57961	ADB58321	ADC99112	AD161656
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36.7	35.9	35.9	35.6	35.6	35.6	34.1	34.1	34.0	34.0	33.5	33.3	33.3	32.9	32.9	32.4	29.9	29.6	29.6	29.6	26.2	24.6	24.5	24.5
601.2	587.8	587.8	582.2	582.2	582	557.2	557.2	557	557	547.6	545.4	544.8	538.8	538.8	529.4	489	485	485	485	428	402.4	400.8	400.8
21	33	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss. Arabidopsis thaliana DNA fragment SEQ ID NO: 54312. AAC47571 standard; DNA; 1501 BP. 99US-0121825P.
99US-0123180P.
99US-0125384P.
99US-0126264P.
99US-0126264P.
99US-012624P.
99US-0128234P.
99US-012845P.
99US-0130449P.
99US-0130449P.
99US-0130449P. 99US-0132485P. 99US-0132486P. 99US-0132487P. 25-FEB-2000; 2000EP-00301439 99US-0132048P. (first entry) Arabidopsis thaliana EP1033405-A2. 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 18-OCT-2000 06-SEP-2000. 06-MAY-1999 19-APR-1999 AAC47571; 

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                                     TACTICTIGGGCAGCCGTTATICCCGGGAGAAAATTCTGTGGACCAGCTAGTGGAGAAGATC
                                                                                                                                                    961 ACTTCAGATTCCCACAAATCAAAGCCCACCTTGGCATAAGGTTTTCCACAAAGCGGATGC
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                                                                                                                                                                                                                                                                    Gaps
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99US-0160980P.
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Matches 1488; Conservative
22-0CT-1999;
22-0CT-1999;
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                                                               ATCCCCTCACCCATCAGTGTAAGCTCTGTGTATTTTGGAAGTGCAAAAGTACTGGTGAAAG
                                                                                         GTGCCACAGAGTATACATCATCATTGATATATGGTCTGCTTGTTGTTCTGGCAGAGC
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Best Local Similarity 99.3%; Pred. No. 5.8e-214;
Matches 1484; Conservative 0; Mismatches 10;
         990S-0159294P-
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protein ic promoter; Arabidops; EP1033405	PR 25-FEB-2000; XX

OY 369 TATAAAACCGAGAGTTGCAATTAATGCGACTAATGGACCATCCAAATGTGGTTTCCTTG 428	dy         429         AAGCALTGITTCTCTACAACAACTAGAGATGAGCICTTCCTCAATCTCGTTATGGAG         488           Db         422         AAGCACTTTCTTCTTACTACAACTAGAGATGAGATCAACCTTTCCTCAACCTTTTTTTT	489 TATGTACCAGGATTTGTACCGGGTTTTGAAGCACTATACTAGTTCAAACCAGCGGATG		Qy 609 ACTGCTCCTGGTGTCTGCCACAGAGATATAAAACCACAAAATCTTTTGGTTGATCCCCAC 668	Qy 669 ACCCATCAGTGTAAGGTCTGTGATTTTGGAAGTGCAAAAGTACTGGTGAAAGGTGAACCA 728	OY 729 AACATATCATATATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGCCACA 788	OY 789 GAGTATACATCATCCATTGATATATGGTCTGGTTGTGTTGTGGAGCTACTTCTT 848	QY         849         GGGCAGCCGTTATTCCCGGAGAAATTCTGTGGACCAGCTAGTGGAGATCATAAAGGTT         908	Oy 909 CTIGGTACTCCAACTGGGAAGAATCGGTGCATGAACCCAAACTACACAGACTTCAGA 968	OY 969 TTCCCACAAATCAAAGCCCACCCTTGGCATAAGGTTTTCCACAAGCGGATGCCTCCGGAA 1028 		1089 GAGGCATGTGCGCATCCGTTTTTCAATGAACTCCGTGAGCCAAATGCTCGTCTTCCAAAT  1082 GAAGCATGTGCTCATCCGTTTTTCAATGAACTCCGAGGCCAAAGGCCCACGTCTTCCAAAT	1149 GSCCGACCTCTACCACCGTGTCCAACCAGGGTTCTCTGGGGCTTCACCGGGGGTTCACCGGGGGGGG	CTTATCAACAGGCTAATACCAGAGCATGTGAGGCGACAGATGATGGTGGCTTTCCATTT	1269 CAAGCTGGACCTAGAAAGCGATCTCGAGATGCTTTTCCAGAGCAAAATGCCGCCTTAT	1319	Db 1377CCGTAGTAAAGTCATATTCAGCTTTTTGAGAAATCAGATA 1422
07-SEP-1999; 10-SEP-1999; 13-SEP-1999; 15-SEP-1999;	16-SEP-1999; 20-SEP-1999; 22-SEP-1999; 23-SEP-1999;	24-SEP-1999; 28-SEP-1999; 29-SEP-1999; 04-OCT-1999;	05-OCT-1999; 06-OCT-1999; 07-OCT-1999; 08-OCT-1999;	12-OCT-1999; 13-OCT-1999; 13-OCT-1999; 13-OCT-1999;	14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999;	14-0CI-1999; 18-0CI-1999; 21-0CI-1999; 21-0CI-1999;	21-0C1-1999; 21-0CT-1999; 21-0CT-1999; 21-0CT-1999;	22-0CT-1999; 22-0CT-1999; 22-0CT-1999; 25-0CT-1999;	25-0CI-1999; 25-0CI-1999; 26-0CI-1999; 26-0CI-1999;	FR 28-OCT-1999; 99US-0161920P.  PR 28-OCT-1999; 99US-0161920P.  PR 28-OCT-1999; 99US-0161931P.  PR 28-OCT-1999; 99US-0161931P.  PR 29-OCT-1999; 99US-0162142P.	Duery Match Best Local Similar Atches 1224; Con	9 TTCAGTGAGAGAGAGTTAGAGCTGTAAAAGCACATGACTTCGATACCATTGG 	Oy         69 CCTCAGCCTCCTCTAGCTCCTCAGCCGCACATCTTCACGGCGGAGATTCTTTGAAA 128           D         68 CAGCCTCATGCTCTTGCTCCGCCGCTTCACGACGCCACGCTTTGAAA 121	ATGAT      ATGAC	Oy 189 GCTGTTACCGGTCACATAATTTCTACTACAATTGGAGGCAAAATGGTGAACCTAAACAG 248  Db 182 GCTGTTACTGGTCATATTCCACTACTATGAGGAGGAAAACGGCGAACCAAAGGG G 241	OY 249 ACCATTAGTTACATGGCCGAACGTGTTGTTGGAACAGGATCATTCGGATTGTATTCCAG 308	Oy 309 GCAAAATGCTTGGAAAACTGGAGAATCAGTAGCCATTAAGAAGGTTTTGCAAGATCGCCGT 368 

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GGCCGACCTCTACCACCGTTGTTCAACTTCAAACAAGAGTTGTCTGGGGGCTTCACCGGAG 1208
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                                                                                  GCTGTTACCGGTCACATAATTTCTACTACAATTGGAGGCAAAAATGGTGAACCTAAACAG
                                                                                                                                                                                                                                                                     GCAAAATGCTTGGAAACTGGAGAATCAGTAGCCATTAAGAAGGTTTTGCAAGATCGCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a full-length cDNA encoding GmPK-3, a novel soybean protein kinase stress-related polypeptide (PKSRP). The cDNA was identified on the baais of homology to PNyscomitrella patens PK-3 (see ACC57962) and PK-10 (see ACC57966) sequence. GmPK-3 is an example of PKSRPB of the invention that are important for modulating a plant's response to environmental stress. Over-expression of PKSRP coding nucleic acids in a plant results in the plant's increased tolerance to environmental stress. Transgenic monocot and dicot plants are provided that show increased tolerance to high salinity, drought and low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New protein kinase stress-related polypeptide coding nucleic acid, useful for producing transgenic plants with an increased tolerance to an environmental stress, e.g. high salinity, as compared to a wild type
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47.4%; Score 775.2; DB 8; Length 1744;
Best Local Similarity 79.4%; Pred. No. 4.4e-108;
Matches 918; Conservative 0; Mismatches 238; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soybean protein kinase stress-related polypeptide GmPK-3 cDNA
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   1228 CTGATCAATAGGCTCATCCCGGAGCATATTAGGCGGCAGATGGGTCTCAGCTTCCCGCAT 1287
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                                                                                                                          Arabidopsis thaliana DNA fragment SEQ ID NO: 55886.
                                                                             AAC47997 standard; DNA; 1657 BP
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The mutant polypeptide comprises at least 70 % sequence identity to the amino acid sequence of the DWF12 polypeptide given in the specification to a positions 38-326 or 1-380, and having a mutation of at least one nonconservative substitution, addition or deletion of an amino acid in a cepton of the polypeptide corresponding to a region given in the specification. The mutant DWF12 polypeptide is useful in producing transgenic plants that display at least one altered DWF12 phenotype, such as altered blochemistry, structure or morphology. The transgenic plant can be used in plant breeding or directly in agricultural production or industrial applications. The polymedicetide is useful in isolating or creating other mutant cell gene alleles, in inhibiting or enhancing candogenous DWF12 gone expression, and in standard diagnostic assays as hybridisation probe or primer. This polymuclectide sequence represents the cDNA of the wild-type DWF12 locus of the invention
                                                                                                                                                                                                                                                                                                                                                                                     DWARF12; DWF12; transgenic plant; plant breeding; industrial application; agricultural production; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated DWARF12 mutant polypeptide for producing transgenic plants displaying altered biochemistry, structure or morphology which are useful in plant breeding, in agricultural production or industrial applications.
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Pred. No. 1e-101;
0; Mismatches 260; Indels 0
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/product= "Protein of wild-type DW12 locus"
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200. .1312
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                                                                                                                                                               standard; cDNA; 1490 BP.
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P-PSDB; AAO26726, AAO26727.
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18-AUG-1999
   Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 52951
                                                                       AAC47206 standard; DNA; 1745 BP
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 TTCTCTACAACGACTAGAGATGAGCTCTTCCTCAATCTCGTTATGGAGTATGTACCAGAG
                                                                                                                                                                         AAGCTCTGTGATTTTGGAAGTGCAAAAGTACTGGTGAAAGTGAACCAAACATATCATAT
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                                                                                              GTCAAACTTTACACATACCAAATCTTCAGAGGCTTGGCTTATATCCATACTGCTCGGT
                                                                        ACATTGTACCGGGTTTTGAAGCACTATACTAGTTCAAACCAGCGGATGCCTATCTTAT
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growth regulator; animal feed product; thale cress;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid arrepresentative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell stress response. The method is useful in the production of transgenic plants, cells me method is useful in the production of transgenic plants, cells me method is useful in the production of transgenic plants contact and stress. The present sequence is that of an Arabidopais thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACATAATTTCTACTACAATTGGAGGCAAAATGGTGAACCTAAAACAGACCATTAGTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGCCGAACGTGTTGGAACAGGATCATTCGGAATTGTATTCCAGGCAAAATGCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGTTGCAATTAATGCGACTAATGGACCATCCAAATGTGGTTTCCTTGAAGCATTGTTTC
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44.7%; Score 730.8; DB 6; Length 1143;
Best Local Similarity 77.5%; Pred. No. 2.2e-101;
Matches 885; Conservative 0; Mismatches 257; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 144; SEQ ID NO 875; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;
                                                                                                                                                   Arabidopsis thaliana; plant; gene; stress; transgenic; ds
                                                                                                                Arabidopsis thaliana stress regulated gene SEQ ID NO 875.
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
 DNA; 1143
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                                                                            entry)
                                                                                                                                                                                         Arabidopsis thaliana
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 standard;
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**AAGCTCTGTGATTTTGGAAGTGCAAAAGTACTGGTGAAAGGTGAACCAAACATATCATAT** 

GTCTGCCACAGAGATATAAAACCACAAAATCTTTTGGTTGATCCCCACCCCATCAGTGT

541 AAAATCTGTGACTTTGGCAGTGCGAAACAGCTCGTTAAAGGTGAAGCCAACATTTCTTAC 600

ATCTGCTCACGATTCTACCGTGCACCCGAGCTCATATTTGGTGCCACTGAGTACACAACT 660

601

801 661 861 721 921 781 981 841

741

TCTATTGATATCTGGTCTGCTTGTGTTTCTTGCTGAGCTTCTTCTTGGTCAGCCATTA

**TTCCCGGGAGAAATTCTGTGGACCAGCTAGTGGAGATCATAAAGGTTCTTGGTACTCCA** 

ATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGCCACAGAGTATACATCA

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860 720 920 780

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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up cardown-regulated in transgenic plants overspressing the heterodimeric E2Fa/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, siress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, cach relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, ell wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polynucleotide sequence is thale cress cDNA capacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                       Altering plant characteristics, useful for producing plants for enzyme pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACATAATTTCTACTACAATTGGAGGCAAAAATGGTGAACCTAAACAGACCATTAGTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 730.8; DB 12; Length 1143; Pred. No. 2.2e-101;
cell wall biosynthesis; nitrogen metabolism; carbon metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;
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                                                                                                                                                                20-OCT-2003; 2003WO-EP011658
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Best Local Similarity 77.5%;
Matches 885; Conservative
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                                        Arabidopsis thaliana
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P-PSDB; ADN73385.
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AAAGCCCACCCTTGGCATAAGGTTTTCCACAAGCGGATGCCTCCGGAAGCCATTGACCTT 1040

ACTCGCGAAGAAATCCGGTGCATGAACCCAAACTACACAGACTTCAGATTCCCACAAATC 980

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ACTCGAGAAGAAATCCGTTGTATGAATCCACATTACACAGATTTCAGGTTTCCACAGATA

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GCATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCA

CATCCGTTTTTCAATGAACTCCGTGAGCCAAATGCTCGTCTTCCAAATGGCCGACCTCTA 1160 CATCCGTTCTTTGATGAACTCAGAGAACCAAACGCTCGTTTACCAAATGGACGGCCTTTC 1020 CCACCGTTGTTCAACTTCAAACAAGAGTTGTCTGGGGGCTTCACGGGAGCTTATCAACAGG 1220 CCGCCTCTCTTCAACTTCAACAAGAAGTAGCTGGATCATCACCTGAACTGGTCAACAAG 1080 CTAATACCAGAGCATGTGAGGCGACAGATGAATGGTGGCTTTCCATTTCAAGCTGGACCC 1280 

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                    Arabidopsis thaliana DNA fragment SEQ ID NO: 33613.
                                                                                                                         BP.
                                                                                                                         AAC41916 standard; DNA; 1635
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                                     ATGCCCGAACGTGTTGGAACAGGATCATTCGGAATTGTATTCCAGGCAAAATGCTTG
                                                                                                            GAAACTGGAGAATCAGTAGCCATTAAGAAGGTTTTGCAAGATCGCCGTTATAAAAACCGA
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               30 - 70N - 1999 | 01 - 70L - 1999 | 02 - 70L - 1999 | 06 - 70L - 1999 | 06 - 70L - 1999 | 06 - 70L - 1999 | 13 - 70L - 1999 | 13 - 70L - 1999 | 14 - 70L - 1999 | 15 - 70L - 1999 | 19 - 70L - 1
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                 Arabidopsis thaliana
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  575 GATCTTCAGAGGACTTGCTTACATTCACAATGTTGCTGGAGTTTGTCACAGAGATCTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a full-length cDNA encoding BnPK-2, a novel canola protein kinase stress-related polypeptide (FKSRP). The cDNA was identified on the basis of homology to Physcomitrella patens FK-3 (see ACC57962) and FK-10 (see ACC57966) sequence. BnFK-2 is an example of PKSRPB of the invention that are important for modulating a plant's response to environmental stress. Over-expression of PKSRP coding nucleic acids in a plant results in the plant's increased tolerance to environmental stress. Transgenic monocot and dicot plants are provided that show increased tolerance to high salinity, drought and low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340
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                                                                                                                                                                                                                                                                                                                                                                           New protein kinase stress-related polypeptide coding nucleic acid, useful for producing transgenic plants with an increased tolerance to an environmental stress, e.g. high salinity, as compared to a wild type variety of the plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACATTACAGCACTGCTAACCAGAGGATGCCGCTTGTTTATGTTAAACTCTATATGTACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACAGGATCATTCGGAATTGTATTCCAGGCAAAATGCTTGGAAACTGGAGAÁTCAGTAGC
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Pred. No. 4.2e-98;
0; Mismatches 265; Indels
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ilarity 76.6%;
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                                                                                                                                                                                                                                                                                                      ATATCAAAGCTCATCCTTGGCATAAGGTTTTTCACAAGCGAATGCCTCCTGAAGCAATTG
                                                                                                                                                               CTTGTTCCCAGGAGAAATCAGGTTGACCAACTCGTGGAAATTATCAAGATTCTTGCA
                                                                                                                                                                                                              CTCCAACTCGCGAAGAAATCCGGTGCATGAACCCAAACTACACAGACTTCAGATTCCCAC
                                                                                                                                                                                                                                    CTCTACCACCGTTGTTCAACTTCAAACAAGAGTTGTCTGGGGGCTTCACCGGAGCTTATCA
 CATATATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGCCACAGAGTATA
                    CATACATATGTTCACGGTACTATCGTGCCCCAGAGCTAATATTTGGTGCGGCAGAATACA
                                                                                                                                         CGTTATTCCCGGGAGAAATTCTGTGGACCAGCTAGTGGAGATCATAAAGGTTCTTGGTA
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                                                                     CATCATCCATTGATATATGGTCTGCTTGTTGTTCTTGGCAGAGCTACTTCTTGGGCAGC
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                               ATCAGCTICITGAGATAATAAAGGTTCTTGGTACCCCAACGCGCGAGGAAATCCGATGTA
                                                                 TGAACCCAAACTACACAGACTTCAGATTCCCACAAATCAAAGCCCACCCTTGGCATAAGG
                                                                                                                 TTTTCCACACAGGGGATGCCTCCGGAAGCCATTGACCTTGCATCTCGGCTTCTTCAATACT
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                                                               The invention relates to protein kinases, especially calcium-dependent phosphorylase kinase (CDEK) and glycogen synthase -3 (GSK-3). The polypeptides having GSK activity can be expressed by standard recombinant methodology. The polymucleotides encoding the polypeptides are useful for isolating cDNAs and genes encoding homologous proteins from the same or other plant species, for immunological screening of cDNA expression libraries, and for creating transgenic plants in which the glycogen synthase kinase polypeptides are present at higher or lower levels than normally found. The polynucleotides are also useful as probes for genetically and physically mapping the genes that they are part of, and smarkers for traits linked to those genes that they are part of, and for altering the level of expression of GSK-3 in a transformed host cell. The present sequence represents a wheat GSK-3 CDNA
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   Col 45-48; 42pp; English
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1044 1016 1104 1164 1136 1017 ccciscorricaccagrarricaccaaarcracerricaccacricardargcaricacarrar 1076 CGTTGTTCAACTTCAAACAAGAGTTGTCTGGGGCTTCACCGGAGCTTATCAACAGGCTAA 1224 The present invention describes kinase polypeptides (I) such as a calcium dependent phosphorylase kinase polypeptide comprising a sequence of 101, 623, 157 or 111 (see ABP53629 to ABP53632) amino acids, and a glycogen synthase kinase polypeptide comprising all or a portion of a sequence of Glycogen synthase kinase; kinase; enzyme; plant; immunological screening; glycogen synthase kinase of kinase polypeptides in CAGGAGAGACTGCGGTTGATCAGCTAGTGGAGATTATCAAGGTTCTTGGTACTCCAACCC GCGAAGAATCCGGTGCATGAACCCAAACTACACAGACTTCAGATTCCCACAAATCAAAG CTCATCCTTGGCACAAGATTTTCCACAAGAGAATGCCCGCTGAAGCTATAGATCTTGCCT CTCGGCTTCTTCAATACTCACCAAGTCTACGTTGCACTGCGCTCGAGGCATGTGCGCATC CGITITICAAIGAACICCGIGAGCCAAAIGCICGICTICCAAAIGGCCGACCICTACCAC 1077 CCTTCTTTGATGAGCTACGTGAGCCGAATGCACGCTTGCCGAATGGCCGCCCATTCCCTC CCCACCCTTGGCATAAGGTTTTCCACAAGCGGATGCCTCCGGAAGCCATTGACCTTGCAT Wheat glycogen synthase kinase encoding cDNA SEQ ID NO:15 /product= "glycogen synthase kinase" New calcium-dependent phosphorylase kinase and polypeptides, for altering level of expression plants. TACCAGAGCATGTGAGGCGACAGA 1248 1197 TTCCGGAACATGTTCGACGCAAA 1220 Claim 15; Page 22-24; 41pp; English. Location/Qualifiers B ABQ82534 standard; cDNA; 1673 98US-0092438P. 14-MAY-2001; 2001US-00854731 (first entry) plant breeding; gene; ss WPI; 2002-731384/79.

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cc useful for immunological screening of CDNA expression libraries, and for useful for immunological screening of CDNA expression libraries, and for preparing antibodies against the polypetides, where the antibodies would be useful for detecting (I) in situ or in vitro, in cell extracts.

CC Nucleic acids (II) encoding (I) can be used to isolate CDNAs and genes can also be used for creating transgenic plants in which (I) is present at higher or lower levels than normal or in cell types or in developmental stages in which they are not normally found. (II) are useful as probes or primers. The polymucleotides may be used as probes for grainst for genetically and physically mapping the genes that they are a part of and used as markers for traits linked to those genes. The information can be used in plant breeding in order to develop lines with desired the present invention phenotypes. The preser the present invention 88888888888888888888888888

Sequence 1673 BP; 419 A; 421 C; 408 G; 424 T; 0 U; 1 Other;

	Ö	204	176
	0; Gaps	GTCACA	GTCACA
1673;		TTACCG	TGACCC
Length	Indels	ATGATGCTC	ACGACGCC
DB 6; e-92;	273;	AAGGAAZ	AGGGGA
40.8%; Score 667.2; DB 6; Length 1673; 75.3%; Pred. No. 8.38-92;	; Mismatches 273; Indels	145 ACAACGACAAGGAAATGTCTGCTGCTGTTATAGAAGGAAATGATGGTGTTACCGGTCACA 204	117 AGAAGCAGCAGGAGGCGAGGCGCCGTATGCGGAGGGAAACGACGCCATGACCGGTCACA 176
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Query Match Best Local Similarity	Matches 831; Conservative	ACAACGACAA	AGAAGCAGCA
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GCCACAGGGATGTGAAACCACAAAATGTTTTTGGTTGATCCTCTAACCCATCAAGA GCCACAGAGATATAAAACCACAAAATCTTTTGGTTGATCCCCACACACCCATCAGTGAAGC TCTGTGATTTTGGAAGTGCAAAAGTACTGGTGAAAGGTGAACCAAACATATCATATCT 597 685 625

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GCTCTCGCTACTATCGTGCTCCTGAGCTCATATTTGGTGCAACTGAATATACAACTTCAA GCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGCCACAGAGTATACATCATCCA 657 745 717 TTGATATATGGTCTGCTGGTTGTGTTCTGGCAGAGCTACTTCTTGGGCAGCCGTTATTCC

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1044 1016 1076 1164 1136 CGTTGTTCAACTTCAAAGAGTTGTCTGGGGCTTCACCGGAGCTTATCAACAGGCTAA 1224 CTCTGTTCAACTTCAAACCTGAACTAGCGAACGCCTCTCCAGAGCTCATCAACAGGCTTG 1196 CTCGGCTTCTTCAATACTCACCAAGTCTACGTTGCACTGCGCTCGAGGCATGTGCGCATC 1104 926 984 CCCGCCTTCTCCCAGTATTCACCAAATCTACGTTGCACGCTCTTGATGCATGTGCACATT ccricriraniciaecracereaeccanicacerecenseceniaecentesecentesecen GCGAAGAAATCCGGTGCATGAACCCAAACTACACAGACTTCAGATTCCCACAAATCAAAG CCCACCCTTGGCATAAGGTTTTCCACAAGCGGATGCCTCCGGAAGCCATTGACCTTGCAT CICATCCTTGCCACAAGATTTTCCACAAGAGAATGCCCGCTGAAGCTATAGATCTTGCCT CGTTTTTCAATGAACTCCGTGAGCCAAATGCTCGTCTTCCAAATGGCCGACCTCTACCAC TACCAGAGCATGTGAGGCGACAGA 1248 1045 1017 1137 1225 1105 1077 1165 925 985 957 g g 셤 8 g ઠે ઠે ठ ò

Search completed: June 23, 2005, 11:46:58 Job time : 1289.09 secs

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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

June 23, 2005, 10:21:17; Search time 397.52 Seconds (without alignments) 6734.116 Million cell updates/sec

1636 Perfect score:

Sequence:

IDENTITY NUC Scoring table:

Gapop 10.0 , Gapext 1.0

1202784 seqs, 818138359 residues Searched:

2405568 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

		. •			SUMMARIES	
Result		Query				
No.	Score	Match	Length	08	ID	Description
1	1636	100.0	1636	4	US-09-578-194-6	Sequence 6, Appli
8	667.2	40.8	1673	ო	US-09-347-801-15	15,
ო	667.2	40.8	1673	4	US-09-854-731-15	15,
4	557.2	34.1	1814	m	US-09-347-801-9	6
'n	557.2	34.1	1814	4	US-09-854-731-9	6
9	538.8	32.9	1429	ო	US-09-347-801-13	Sequence 13, Appl
7	538.8	32.9	1429	4	US-09-854-731-13	13
œ	400.8	24.5	1952	4	US-09-566-921-24	24,
0	400.8	24.5	2154	m	US-09-488-856A-3	Α,
10	395.6	24.2	1389	m	US-09-489-765A-3	'n
11	395.6	24.2	1389	4	US-09-016-434-1414	141
12	394	24.1	2088	~	US-08-602-264A-1	Ļ
13	394	24.1	2088	ო	US-08-461-018A-1	Sequence 1, Appli
14	394	24.1	2088	m	US-09-216-958-1	Ļ
15	390	23.8	1972	~	US-08-602-264A-2	7
16	390	23.8	1972	m	US-08-461-018A-2	Sequence 2, Appli
17	390	23.8	1972	ო	US-09-216-958-2	~
18	289.6	17.7	1185	4	US-09-248-796A-4396	439
19	174.2	10.6	304	4	US-09-313-294A-6825	Sequence 6825, Ap
20	154	9.4	286	4	US-09-313-294A-2895	289
21	140.2	8.6	305	4	US-09-313-294A-5874	5874,
22	134.6	8.2	1236	4	US-09-248-796A-4397	4397,
23	122.6	7.5	584	m	US-09-347-801-11	11, Aj
24	122.6	7.5	584	4	US-09-854-731-11	Sequence 11, Appl
25	106.4	6.5	275	4	US-09-313-294A-1703	1703
56	101.6	6.2	272	4	09-313-294A-6	6721,
27	96.2	5.9	479	~	US-08-602-264A-13	13,

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Gaps ö

DB 4; Length 1636; 0; Indels

Query Match
100.0%; Score 1636; 1
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1636; Conservative 0; Mismatches

DATE: 1997-01-01
DATABASE ACCESSION NUMBER: genbank/X94938
DATABASE ENTRY DATE: 1998-02-13
RELEVANT RESIDUES: (1)..(1636)

; RELEVANT RE: US-09-578-194-6

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61 TGGGGCCTCCTCAGCCTCCGTCTTTAGCTCCTCAGCCGCCGCATCTTCACGGGGGAGTT

1 TTTACTCTTTCAGTGAGAGAGAGAGTTAGAGCTGTAAAAGCACATGATTCGATACCAT

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TTTACTCTTTCAGTGAGAGAGAAGTTAGAGCTGTAAAAGCACATGACTTCGATACCAT

Sequence 13, Appl Sequence 13, Appl	14,	Sequence 04, Appl	Sequence 9, Appli	Sequence 1, Appil Sequence 89, Appl	158,	Sequence 36, Appl	Sequence 158, App	Sequence 158, App	Sequence 158, App	Seguence 36, Appl	Sequence 158, App		Sequence 158, App	Sequence 158, App
US-08-461-018A-13 US-09-216-958-13	US-09-014-969-14	US-08-621-994-64 US-09-601-537-10	US-09-601-537-9	US-U9-3/U-253-1 US-09-489-847-89	US-09-907-794A-158	US-09-866-028-36	US-09-905-125A-158	US-09-902-775A-158	US-09-906-700-158	US-09-944-457-36	US-09-903-603A-158	US-09-904-920A-158	US-09-909-064-158	US-09-905-381A-158
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96.2	94.6	93.4	93.4	92.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8
28	30	35	33	տ ա	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and Kreis, M. TITLE: Three New cDNAs Related to SGG/GSK-3 ( Shaggy/Glycogen Synthase Kinase-3) TITLE: from Arabidopsis thaliana ( Accession No. 6822139 X94938, x94939 and X99696) TITLE: 008)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mRNA
LOCATION: (1)...(1636)
OTHER INFORMATION: strain Columbia ecotype
OTHER INFORMATION: tissue type leaves
OTHER INFORMATION: tissue type leaves
OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots
PUBLICATION INFORMATION:
        - Instant
                                                                                                    APPLICANT: Sudwestdeutsche Saatzucht-SWS;
APPLICANT: Advanta Seeds B.V.
TITLE OF INVENTION: Modulation of Storage Organs;
FILE REFRENCE: 026-1
CURRENT APPLICATION NUMBER: US/09/578,194;
CURRENT FILING DATE: 2000-05-24;
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 1636
US-09-578-194-6; Application US/09578194; Sequence 6, Application US/09578194; Patent No. 6822139; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Arabidopsis sp.
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL: Plant Physiol. VOLUME: 113
ISSUE: 1
PAGES: 306-306
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Pred. No. 3.3e-141;
0; Mismatches 273;
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/092,438
PRIOR FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SQL ID NO 15
LENGTH: 1673
                                                                                                                                                                                             40.8%;
                                                                                                          TYPE: DNA ORGANISM: Triticum aestivum
                                                                                                                                                                                                        al Similarity 75.3
831; Conservative
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; LOCATION: (1349)
US-09-854-731-15
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Best Local S:
Matches 831
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Patent No. 6794561
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
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Pred. No. 2.4e-116;
0; Mismatches 303;
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Fatent No. 6794561
GENERAL INFORMATION:
APPLICANT: Allen, Steve
FAPLICANT: Allen, Steve
TITLE OF INVENTION: Plant Protein Kinases
FILE REFRENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT APPLICATION NUMBER: 60/092,438
FRIOR APPLICATION NUMBER: 60/092,438
FRIOR APPLICATION NUMBER: 60/092,438
FRIOR APPLICATION NUMBER: 01998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
LENGTH. 1014
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Best Local Similarity 70.9%;
Matches 739; Conservative
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US-09-854-731-9
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; Sequence 9, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
    APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; SOFTWARE: MICTOROFT ONS: 23
; SOFTWARE: MICTOROFT OFFICE 
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Score 538.8; DB 3;
Pred. No. 3.2e-112;
0; Mismatches 304;
                                                                    APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER PILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
                          Sequence 13, Application US/09347801
Patent No. 6262345
GENERAL INFORMATION:
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Best Local Similarity 70.5
Matches 733; Conservative
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ORGANISM: Glycine
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; LOCATION: (1410)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1416)
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LENGTH: 1429
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ATAGACAACGACAAGGAAATGTCTGCTGCTGTTATAGAAGGAAATGATGCTGTTACCGGT
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387 282 283 TIGIGACTACCATIGGGGGTAGAAATGGTCAGCCCCAAGCAGACTATAAGCTACATGGGAG 342 402 447 522 567 327 462 507 AAACAATGCGCCTTCTTGACCACCCAAATGTCGTTGCTTTGAAGCACTGTTTCTTTTCAA 508 ACCGGGTTTTGAAGCACTATACTAGTTCAAACCAGCGGATGCCTATCTTCTATGTCAAC 208 TTTCTACTACTACTAGGAGGCAAAATGGTGAACCTAAACAGACCATTAGTTACATGGCCG **AACGTGTTGTTGGAACAGGATCATTCGGAATTGTATTCCAGGCAAAATGCTTGGAAAACTG** AATTAATGCGACTAATGGACCATCCAAATGTGGTTTCCTTGAAGCATTGTTTCTTCTTCTA CAACGACTAGAGATGAGCTCTTCCTCAATCTCGTTATGGAGTATGTACCAGAGACATTGT 148 ACGACAAGGAAATGTCTGCTGCTGTTATAGAAGGAAATGATGCTGTTACCGGTCACATAA GAGAATCAGTAGCCATTAAGAAGGTTTTTGCAAGATCGCCGTTATAAAAACCGAGAGTTGC Grgaaactgrggcratcaaaaggrtcrtcaagacaagaggracaagaaccgggagcrgc Gaps ä; Length 1429; Indels

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                                                                                                                                                    Length 1429;
                                                                                                                                                                                   Indels
                                                                                                                                                      Score 538.8; DB 4;
Pred. No. 3.2e-112;
0; Mismatches 304;
                                                                                                                                                      Query Match 32.9%;
Best Local Similarity 70.5%;
Matches 733; Conservative
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              LOCATION:
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583 ATCGGGTGATAAAACATTACAACAAGTTTAACCAAAGGATGCCACTGATATGTGAAAC
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                             Arcegeararcaaecercaaarcrarregreaarceaecaecaeceeecaecrraarrar
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                                                                                                                                                                                   APPLICANT: Allen, Steve
APPLICANT: Allen, Steve
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT FILING DATE: 2001-05-14
PRIOR PLICATION NUMBER: 60/092,438
PRIOR FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
LENGTH: 1429
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ORGANISM: Glycine me
FEATURE:
LOCATION: (1202)
NAME/KEY: unsure
LOCATION: (1231)
NAME/KEY: unsure
LOCATION: (1237)
NAME/KEY: unsure
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US-09-854-731-13
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APPLICANT: Brett P. Monia
APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Adequeline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXPRIBER OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXPRIBER OF INVENT APPLICATION NUMBER: US/09/488,856A
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 88
LENGTH: 2154
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                                                                                                                                                                                            861 GTGGGGTGGACCAGCTGGTGGAGATCATCAAGGTGCTGGGAACACCAACCGGAACAAA
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TTGGAAGTGCAAAAGTACTGGTGAAAGGTGAACCAAACATATCATATATCTGCTCTCGGT
                                      681 TTGGCAGTGCAAAGCAGTTGGTCCGAGGGGAGCCCAATGTCTCCTACATCTGTTCTCGCT
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; LOCATION: (92)...(1543)
US-09-488-856A-3
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ORGANISM: Homo sapiens
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US-09-488-856A-3
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APPLICANT: Tingley, Debora W.
APPLICANT: Tingley, Debora W.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISJ.
FILE REFERENCE: PA-0024 US
CURRENT APPLICATION UNMERR: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
SOT WARE: PERL Program
LENGTH: 1952
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; OTHER INFORMATION: Incyte ID No. 6682888 234735.15
US-09-566-921-24 ·
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Patent No. 6682888
GENERAL INFORMATION:
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US-09-489-765A-3; Sequence 3, Application US/09489765A; Sequence 3, Application US/09489765A; Settent No. 6333029; GENERAL INFORMATION:

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APPLICANT: Robert McKay
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRESS
TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRESS
CURRENT APPLICATION NUMBER: US/09/489,765A
CURRENT FILING DATE: 2000-01-19
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 1389
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Madeline M. Butler
                                                                                                                                                                                                                                                                                                         ...(1302)
                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                     ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40).
US-09-489-765A-3
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Sequence 1, Application US/08602264A

Sequence 1, Application US/08602264A

Setent No. 5837853

GENERAL INFORMATION:
APPLICANT: Akihiko TAKASHIMA et al.
APPLICANT: Akihiko TAKASHIMA et al.
TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
TITLE OF INVENTION: Lau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
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                                          320 AGAATCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAACATAGTCCGATTGCGTT 379
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US-08-602-264A-1
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CCATTGACCTTGCATCTCGGCTTCTTCAATACTCACCAAGTCTACGTTGCACTGCGCTCG
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Sequence 1414, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young

APPLICANT: Janice Au-Young

APPLICANT: Officey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESSPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE: HEREWITH
                                                                                                                                                                                          1097 GGCGAGACACCTGCACTTCAACTTCA 1126
                                                                                                                                                              1150, GCCGACCTCTACCACCGTTGTTCAACTTCA 1179
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1414:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1389 base pairs
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Matches 610; Conservative
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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STATE: CALIFORNIA
COUNTRY: USA
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; CLONE: 9529236
US-09-016-434-1414
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US-09-016-434-1414
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                                                                                GGCAGCCGTTATTCCCCGGAGAAAATTCTGTGGACCAGCTAGTGGAGATCATAAAGGTTC
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Batent No. 6071694

GENERAL INFORMATION:
APPLICANT: ALKINICO TAKASHIMA et al.
APPLICANT: ALKINICO TAKASHIMA et al.
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1150 GCCGACCTCTACCACCGTTGTTCAACTTCA 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1673 GGCGAGACACACCTGCACTTCAACTTCA 1702
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,018A
FILING DATE: June 5, 1995
CLASSIFICATION NUMBER: 08/204,091
FILING APPLICATION NUMBER: 08/204,091
FILING DATE: MARCH 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. CHECK, JT.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 2088 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: D.C.
ZIF: 20005.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
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COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 144 mb
COMPUTER: 18M Compatible
COMPUTER: 18M Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
FILING DATE: February 20, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: MARCH 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA to genomic RNA
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24.1%;
Best Local Similarity 65.5%;
Matches 609; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 2008 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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GENERAL INFORMATION:
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CLASSIFICATION:
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Best Local Si
Matches 609;
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                                           Score 394; DB 3; Length 2088;
Pred. No. 1.9e-79;
0; Mismatches 315; Indels
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                                           Query Match 24.1%;
Best Local Similarity 65.5%;
Matches 609; Conservative
   human being
; ORGANISM:
US-08-461-018A-1
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RESULT

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TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS ACAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES: 13
CORRESPONDENESS:
ADDRESSEE: WENDERCYL, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700 Gaps . 9 Length 2088 tch 24.1%; Score 394; DB 3; Length 20 al Similarity 65.5%; Pred. No. 1.9e-79; 609; Conservative 0; Mismatches 315; Indels ...urkESSEE: ADURESS:
...urkESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTY: D.C.
ZIP: 20005
COMPUTED: US/09/216,958 MOLECULE TYPE: cDNA to genomic RNA ORIGINAL SOURCE: PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,018
FILING DATE: Sequence 1, Application US/09216958 Patent No. 6248559 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in
MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1 NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REFERENCE/POCKET NUMBER: TELECOMMUNICATION INFORMATION: INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 2088 base pairs ATTORNEY/AGENT INFORMATION CURRENT APPLICATION DATA
APPLICATION NUMBER: U ORGANISM: human being TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear 8

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Best Local Similarity 64.2%; Pred. No. 1.5e-78;
Matches 620; Conservative 0; Mismatches 340; Indels
                                                                                                                                                                                                      STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGITAL SOURCE:
ORGANISM: rat
                 REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1972 base pairs TYPE: nucleic acid TYPE: double
REGISTRATION NUMBER:
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Patent No. 5873853

GENERAL INFORMATION:

APPLICANT: Akihiko TAKASHIWA et al.

TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE

TITLE OF INVENTION: TAU-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: WENDEROYH, LIND & PONACK

STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                 1373 GACAACCAATATTTCCAGGGGATAGTGGTGGATCAGTTGGTAGAAATAATCAAGGTCC 1432
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OPERATING SYSTEM: MS-DOS
SOFFWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
FILING DATE: February 20, 1996
CLASSIFICATION: 514
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MEDIUM TYPE: 144 mb
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APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
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US-08-602-264A-2
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Search completed: June 24, 2005, 07:03:27 Job time : 402.52 secs



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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KVLVKGEPNISYICSRYYRAPELIFGATEYTASIDIWSAGCVLAELLLGQPLFPGENS
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LQXSPSCLRCTALLSGCAHFFNELREPNARLPNGKPPLPPFFKQELGGSASELINKLI
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100.0%; Score 1614;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1614; Conservative 0; Mismatches
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Arabidopsis thaliana
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1572)
1 (bases 1 to 1572)
2 (bases 1 to 1572) 900 960 960 900 Hwang I.
An Arabidopsis GSK3/shaggy-like gene that complements yeast salt stress-sensitive mutants is induced by NaCl and abscisic acid Plant Physiol. 119 (4), 1527-1534 (1999) 1501 ACTGTTCCTCGTGTATTTTGTATATGTTTTGTCTGTAAACAATTCTGACAGATACGT TGTATGAACCCGAACTACACAGATTTTAGGTTCCCACAAATCAAAGCTCACCCTTGGCAC TATTCACCAAGTCTACGCTGCACTGCGCTCGAAGCATGCTCCTCCGTTTTTCAATGAA TATTCACCAAGTCTACGCTGCACTGCGCTCGAAGCATGTGCTCCATCCGTTTTTCAATGAA CTCCGAGAGCCAAACGCCCGTCTTCCAAATGGTCGTCCATTACCGCCATTGTTCAATTTC AGACGACAAATGAGCACAGGATTACAAAACAGTTAAAAAACTGTGCATGTCTGAAGAGAAAA GAGGAGAAAAGCAGGTTTACTACTTTTATTTGATAGTTGACAGGTTCAACAGTATATTAA GCTGGTTGTGTACTGGCAGAGCTTCTTCTTGGCCAGCCGTTATTTCCAGGAGAAAATTCA GTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCGTGAAAATTCGA TGTATGAACCCGAACTACACAGATTTTAGGTTCCCACAAATCAAAGCTCACCCTTGGCAC AAACAAGAGTTAGGTGGAGCTTCAATGGAGCTAATCAACAGGCTAATACCTGAGCATGTG 1501 ACTGTTCCTCGTGTATTTTTGTATATGTTTTTGTCTGTAAAACAATTCTGAGATACGT GITGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCGTGAAGAAATTCGA **AGACGACAAATGAGCACAGGATTACAAAACAGTTAAAAACTGTGCATGTCTGAAGAGAA** 1614 

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PENTERED 1019912  TITLE State 10.1572) PLANK T., Lim J.H., Kang S.G., Jin J.B. and TITLE State 10.1572) PLANK MORES PARTIES TO CHARGE 10.1572) PLANK MORES PARTIES TO CHARGE 10.1572 PLANK MORE PARTIES AND CHARGE 10.1571 PLANK MORE PARTIES AND CHARGE 10.1572 PLA	588 541 648 601 708 721	AGAIATATGGTCTGCTGGTTGTGCGGGGGGCTTCTTCTTGGCGGGCGTTATTTCC 81 AGAIATATGGTCTGCTGGTTGTGTACTGGCGGGGGCTTTCTTGGCCGGCGGCGTTATTTCC 81 AGAGAAAATTCAGTTGATGGTGTTGTGGAGGTTCTTGGTACTTCTGGTACTTCCTGGTATTTCC 84 AGGAGAAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCG 94 TGAAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCG 96 TGAAGAAATTCCATTGATGAACCCGAACTACACAGATTTTAGGTTCCCACAAATCAAAGC 10 TGAAGAAATTCGATGTTTTCATAAAACGGATGCCTCCAGAAGCAAATGAACCTTGCATC 10 TCACCCTTGGCACAAGGTTTTTCATAAAACGGATGCCTCCAGAAGCAATAGACCTTGCATC 10 TCACCCTTGGCACAAGGTTTTTCATAAAACGGATGCCTCCAGAAGCAATAGACCTTGCATC 10	1068 TGGGCTTCTTCAATATTCACCAAGTCTACGCTGCACTGCGCTCGAAGCATGTGCTCATCC 1127 1021
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BENGE BENGE CDS BOOM BENGE BEN	10198112 2 (bases 1 to 1572) Piao, H.L., Jang, H.J., Pih, K.T., Lim, J.H., Kang, S.G., Jin, J. Hwang, I. By Submission Direct Submission Submitted (18-MG-1997) Plant Molecular Biology and Biotec Research Center, Gyeongsang National University, Chinju 66 Korea Location/Qualifiers 1. 1572 / organism="Arabidopsis thaliana" / drain="Columbia" / db_xrefe="taxon:3702" 1. 1572 / orgene="GSK1" / notes a calcineurin mutation / notes = "Complements the yeast calcineurin mutation		### 197.1#; Score 1567; DB 8; Length 1572;  Conservative 0; Mismatches 0; Indels 0; Gaps  Madgadadacative 0; Mismatches 0; Indels 0; Gaps  Madgadadacatrcacacatrcacatrcatrcatrcatrcacatrcaccatr

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GACCATTAGITACAIGGCIGAGCGGGTIGITGGAACAGGTTCATICGGGATIGITITTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 GGCGAAATGCTTGGAAACTGGAGAATCAGTAGCCATTAAAAAGGTCTTGCAAGATCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GGCGAAATGCTTGGAAACTGGAGAATCAGTAGCCATTAAAAAGGTCTTGCAAGATCGACG
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/replace="tta"
misc_difference 1567
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6
                                          product="putative shaggy kinase"
protein_id="AAK5953.1"
db_xref="G1:14334750"
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Pred. No. 0;
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                        evidence=experimental
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/gene="At1g06390"
: 1441. .1442
/gene="At1g06390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="At1g06390"
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Best Local Similarity
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                                                 AY035048 116-SEP-2002
Arabidopsis thaliana putative shaggy kinase (Atlg06390) mRNA,
                                                                                                                                                                                                                                                                                                                        1 (Dases I to 1582)
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,
Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Lin, J., Miranda, M., Karlin-Peumanni G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,
Bavis, R.W., Ecker, J.R. and Theologis, A., Shinozaki, K.,
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X., Sakano,H., Pham, P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (03-MAY-2001) Plant Gene Expression Center, 800 Buchanan Submitted (03-MAY-2001) Flant Gene Expression Center, 800 Buchanan RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers
                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Buparmatophyta, Magnollophyta, eudicotyledons, core eudicots,
roaids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 1582)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
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/note="This clone is in a modified pBluescript vector
(FLC-1) as a BamHI/XhoI insert."
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/note="contains an eukaryotic protein kinase PF|00069
domain"
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                                                                                                                                                                                       Arabidopsis thaliana (thale cress)
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/db_xref="taxon:3702"
/chromosome="1"
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/gene="At1g06390"
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SOURCE
ORGANISM
                                                                     DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theologis, A.

Direct Submitssion
Submitted (102-AUG-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakuraal, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                      Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Ondera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y. Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koseema, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Paln, C.J., Meyers, M.C., Miranda, M., Narusaka, M., Suth, M., Paln, C.J., Sakurai, T., Satou, M., Scki, M., Shinn, P., Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Janag, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin, Neumann, G., Kim, C., Kossema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tracy, S.E., Davis, R.W., Ecker, J.R. and Theologis, A.
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1255)
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Etgu, P.,
Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H.,
Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M.,
Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and
                                                                                                                                                                                                     Theologis,A.
Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
2 (bases 1 to 1255)
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/protein_id="AAK33730.1"
/db_xref="GI:15293239"

    1255
    organism="Arabidopsis thaliana"

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/note="contains an eukaryotic
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/note="This clone is in
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/db_xref="taxon:3702"
/chromosome="1"
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/gene="At1g06390"
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    ORGANISM
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Arabidopsis thaliana putative shaggy kinase (Atlg06390) mRNA,
complete cds.
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                                                                                                                                                                                                                                                                                                                                                            GTTCCCACAAATCAAAGCTCACCCTTGGCACAAGGTTTTCATAAACGGATGCCTCCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201 GCTAATCAACAGGCTAATACCTGAGCATGTGAGGAGCACAAATGAGCACAGGATTACAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGATAGITGACAGGTTCAACAGTATATTAACCACGACTATTATCAGCTTCTATACCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    781 AGAGTATACAGCATCCATAGATATATGGTCTGCTGGTTGTGTACACAGAGAGCTTCTTCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                GTTCCCACAAATCAAAGCTCACCCTTGGCACAAGGTTTTTCATAAACGGATGCCTCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCAATAGACCTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACTGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGAAGCATGTGCTCATCCGTTTTTCAATGAACTCCGAGAGCCCAAACGCCCGTCTTCCAAA
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/product="shaggy-like kinase dzeta"
/product="shaggy-like kinase dzeta"
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/db_xref="GA1:1225913"
/db_xref="GA1:1225913"
/db_xref="GA1:029010"
/db_xref="CAN09010"
/
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Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud,
Institut de Biotechnologie des Plantes, Centre de Recherches sur
les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405
ORSAY Cedex, FRANCE
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ASK dzeta gene, serine/threonine kinase, shaggy-like kinase dzeta.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008)

Plant Physicol. 113, 306-306 (1997)

2 (bases 1 to 1636)

Dornelas, M.C.
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A.thaliana mRNA for shaggy-like kinase dzeta.
X94938
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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Columbia ecotype"
/th xref="taxon:3702"
/tissue_type="leaves"
/clone_lib="lambda_ZAPII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corresponding genomic sequence: Y09300.
Location/Qualifiers
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1. .1636
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45. .1283
/gene="ASK dzeta"
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/gene="At1g06390"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.

PLN 13-FEB-1998

Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and

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1 (bases 1 to 1591)
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, B., Dale, J. M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jin, J., M., Jin, J., M., Marusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R., Theologis, A. and Ecker, J.R.
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Arabidopsis thaliana At2g30980/F7F1.19 mRNA, complete cds.
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Shint, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,
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NSVDQLVEIIKVLGTPTREEIRCMNPNYTDFRFPQIKAHPWHKVFHKRMPPEAIDLAS
RLLQYSPSLRCTALEACAHPFNELREPNALLPNGRPLPPLFFRFRGGSSPELINR
LIPEHVRRQMNGGFPFQAGP"
                                                                                                                                                                                Submitted (08-APR-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
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                                                                                                                                                                                                                                                                                             RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN trabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J. Bowser, L.C. Chang, E., Dale, J. M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
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Kawai, J., Lam. B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamadaura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAGAGAGAGAAAATTAGACTTTACTCATTGTTCAGTGGTTGAGAGAAAAGAG-TA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="putative shaggy-like protein kinase dzeta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 315; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 962; DB 8; I
Pred. No. 3.7e-229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RAFL05-02-116(R21926)"
/ecotype="Columbia"
80. .1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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/chromosome="2"
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Best Local Simi
Matches 1220;
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                                                                                                                                                     TITLE
JOURNAL
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/product="putative shaggy protein kinase dzeta"
/protein id="AL1.35376.1"
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YLSSNQRMPIFYKKUTYQIPRGLAYIHTAFGVCHRDVKPQNLLVDPLTHQCKLCDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAKVLVKGEANISYICSRYYRAPELIFGATEYTSSIDIWSAGCVLAELLLGQPLFPGE
NSVDQLVEIIKVLGTPTREEIRCMNPNYTDFRFPQIKAHPWHKVFHKRMPPEAIDLAS
RLLQYSPSLRCTALEACAHPFKNELREPNARLPNGRPLPPLFNFKQELSGASPELINR
Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGCCTCATGC-----TCTTGCTCCGCCGCTGCAGCTTCACGACGGCGACGCTTTGAAA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 ACCATTAGTTACATGGCCGAACGTGTTGTTGGAACAGGATCATTCGGAATTGTATTCCAG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 CCTCAGCCTCCGTCTTTAGCTCCTCAGCCGCCCATCTTCACGGCGGAGATTCTTTGAAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 CGTCGTCCCGATATAGACAACGACAAGGAAATGTCTGCTGCTGTTATAGAAGGAAATGAT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 GCTGTTACCGGTCACATAATTTCTACTACAATTGGAGGCAAAAATGGTGAACCTAAACAG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGAAATGCTTGGAAACTGGAGAATCAGTAGCCATTAAAAAGGTCTTGCAAGATCGACGC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCCGTCCTGAATTGGATTCTGATAAGGAAATGTCTGCAGCTGTTATTGAGGGAAATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGTTACTGGTCATATCATTTCCACTACTATAGGAGGCAAAAACGGCGAACCAAAGCAG
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                                                                                                                                                                                                                                                                                             /ecotype="Columbia"
/note="This clone is in a modified pBluescript vector
(Lambda ZAP) as a XhoI/SstI insert."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 TTCAGTGAGAGAGAGTTAGAGCTGTAAAAGCACATGACTTCGATACCATTGGGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCATTAGTTACATGGCTGAGCGGGTTGTTGGAACAGGTTCATTCGGGATTGTTTTTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCACTGTTTCTTCTCTACAACGAGTAGAGATGAGCTCTTCCTCAACCTTGTTATGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCAGTGGTTGAGAGAGAAAAGAG-TAAAAAAGCACATGGCCTCATTACCATTGGGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.1%; Score 954.6; DB 8;
llarity 78.1%; Pred. No. 2.6e-227;
Conservative 0; Mismatches 309;
                                                                                                                                                                                                                                                                  (R11538)"
                                                                                                                                 /organism="Arabidopsis
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/db_xref="taxon:3702"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                  clone="RAFL06-67-J10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LI PEHVRROMNGGFPFQAGP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .53
/gene="At2g30980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="At2g30980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="At2g30980"
                                                                                                                                                                                                                                                                                                                                                                                                                              gene="At2g30980"
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Matches 1196;
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1566)
12 (bases 1 to 1566)
13 Yamada, K., Liu, S.K., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninof, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin, Heuwann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Bavis, R.W., Ecker, J.R., and Theologis, A., Shinozaki, K., Arabidopsis Pull Length cDNA Clones
Lin, Dupublished
                                                                                                                                                                                                                                                                  1510
                                                                                                                                                                                              1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYO64020 1566 bp mRNA linear PLN 18-SEP-2002
Arabidopsis thaliana putative shaggy protein kinase dzeta
(AR2930980) mRNA, complete cds.
GAGATGCTTTTCCAGAGCAAAATGCCGCCTTATGGAATGAAGGAGAGGGGAGATTTACTTC 1390
                                                                                                                                                                                                                                                                                                                                  1538
                                                                                                                                                                                                                                                                                                                                                                                            1511 CACTGACTTGTAGAGAGATACTTTTCTCCTGTATCAGTATTTGTATATGTTTTTGTCCTT 1570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J., M., Goldmaith, A.D., Lee, J.M., Condera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Rarlin-Neumann, G., Xim, C., Koseema, E., Lam, B., Lin, J., Meyers, M.C., Davis, R.W., Ecker, J.R. and Theologis, A. Southwick, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-NOV-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the Collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakuxai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                GACAGGTTCAACAGTATATTAACCACGACTATTATCAGCTTCTATACCCGTAGTAAAGTC
                                                                                                                                                                                              1419 ATATICAGCITITIGAGAAATCAGAIGCIGAIAATIGCGICIATITITITITATICCIT
                                                                                                                                                                                                                                                                                                                           1479 AGCCTGGAGAGAGAGAGACACTGTTCCTCGTGTATTTTTGTATATGTTTTTGTCTGT
                                                                                                                          1391 TCTCTGATTAACTAAGTATCAGCTTCTGAGAAGAGATGATGTCTCCTCCTTAGACGTGGC
                                                                                                                                                                                                                                                              1451 CAATTCAGCTTTTTGAGAAATCAGGAGGCGATGATTGTGTCCTATTATATTCTTTTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLI CDNA.
Arabidopsis thaliana (thale cress)
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AY064020 LOCUS DEFINITION

RESULT

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

TITLE

COMMENT

210

96 11

Gaps

26;

Length 1566; IndelB 270

330

377

450 437 510 497 TATGTACCTGAGACTTTATACCGGGTTTTTGAGGCACTATACTAGTTCTAATCAGAGGATG 570

511

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Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

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Direct Submission

Submitted (11-MRR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5-truncated; less than one percent are 3-truncated; approximately two percent represent alternative splice variants including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the general considered to be 3'-truncated if it lacks the sequence are cerived from the Ws or Lace coctypes and therefore may contain polymorphisms when compared to sequences from COl-0. Genset carried out the library production and sequences from COl-0. Genset carried out the library production and sequenceing of the full-length clones. Ceres, Inc. carried out the clustering of the location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGNDAVTGHIISTTIGGKNGEPKÖTISYMAERVVGTGSFGIVPQAKCLETGESVAIKK
VLQDRRYKRARELQLMRLMPHVVSLAGFFFGTTRDELEFLANIVMEYVBETLYRVLKH
YTSSNQRMPIFYVATYOTFRGLAYTHTAELEFLANIVMEYVBETLYRVLKH
YTSSNQRMPIFYVATYOTFRGLAYTHTAEPECHTNOFLANIVENLLJGOPLLOFG
SAKVLVKGEANISYICSRYTRSPELIFGATEYTSSIDIWSAGCVLAELLLGOPLFPGE
NSVDBLVBIISTIKKLGTPTREERRENRPNYTDFRRPDIRAPWHKVFHKRMPPBALDLAS
RLLQYSPSLRCTALBACAHPFNGLREPNARLPNGRPLPPLENFKQELSGASPBELINR
LIPEHYRQWNGGFPPQAGP"
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PLN 14-APR-2003
                                                                                                       Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                1 (bases 1 to 1503)
Haas, B.J., Volfdovsky, N., Town, C.D., Troukhan, M., Alexandrov, N.,
Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. Feldmann, K. Fungth cDNA from Arabidopsis thaliana
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  1503 bp mRNA linear PLN:
thaliana clone 36479 mRNA, complete sequence
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Pred. No. 2.1e-226;
0; Mismatches 170; Indels
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                                                                                      GI:21406280
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Best Local Similarity 85.9%;
Matches 1080; Conservative
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacees, Arabidopsis.

E (bases 1 to 1270)

Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Donger, T., Canimi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamitay, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Mayers, M.C., Miranda, M., Natusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Arabidopsis Open Reading Frame (ORF) Clones

Unpublished

Unpublished

E (bases 1 to 1270)

E Chang, M. C., Chang, C. H., Chang, E., Dale, J. M.
                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana putative shaggy protein kinase dzeta (At2g30980) mRNA, complete cds.
1158 GGCCGACCTCTACCACCGTTGTTCAACTTCAAACAAGAGTTGTCTGGGGGCTTCACCGGAG 1217
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The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA : 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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Location/Qualifiers
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                                                                                    Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (/PGEC) contributed equally to this work as PIs.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/db xref="taxon:3702"
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SAKVLVKGEANISYICSRYXRAPELIFGATEYTSSIDIWSAGCVLAELLGGPLFPGE
RLQYSPSLACTALEBERCANPRTDFRPRIFFRETREPPARTDLAS
RLLQYSPSLACTALEBCAHPFNBLREPNARLPNGRPLPPLFNFKQELSGASPELINR
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larity 87.6%; Pred. No. 8.3e-225;
Conservative 0; Mismatches 146;
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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KEYWORDS
SOURCE
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Syngenta Participations

Harper,J.F., Kreps,J., Wang,X. and Zhu,T. Stress-regulated genes of plants, transgenic plants same, and methods of use Patent: WO 0216655-A 875 28-FEB-2002; The Scripps Research Institute (US); Syngenta Parti.

Location/Qualifiers

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                                                                                            Length 1143;
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                                                                                           44.0%; Score 710.4; DB 6; 77.1%; Pred. No. 2.6e-166;
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1. .1143
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Best Local Similarity 77.1
Matches 864; Conservative
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Sequence 875 from Patent WO0216655. AX506180 AX506180.1 GI:23387417

AX506180 LOCUS DEFINITION ACCESSION VERSION

RESULT 11

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114 AAATCTGTGACTTTGGCAGTGCGAAACAGCTCGTTAAAGGTGAAGCCAACATTTCTTACA
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Pred. No. 2.5e-166;
0; Mismatches 256;
                                                                                      thaliana"
                                                                                      organism="Arabidopsis"
                                                                                                        /mol_type="mRNA"
/db_xref="taxon:3702"
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173. .1315
                                                                                                                                                                                               codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.1%;
Matches 864; Conservative
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This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 9'-truncated if it lacks the translation initiation start (ATG).
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                                                                                                                                                     1004 AAGCTCACCCTTGGCACAAGGTTTTTCATAAACGGATGCCTCCAGAAGCAATAGACCTTG 1063
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                                                                                                                                                                                                                                                                                                                                                  962 ATCCGTTCTTTGATGAACTCAGAGAACCAAACGCTCGTTTACCAAATGGACGGCCTTTCC 1021
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                                                                                                                                                                                                                                                                                 902 CATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCAC 961
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Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
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Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N.,
Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
CTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTAGGTTCCCACAAATCA
                                                                                                                                                                                                                                         CATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACTGCGCTCGAAGCATGTGCTC
                                                                                                          782 CTCGAGAAGAAATCCGTTGTATGAATCCACATTACAGATTTCAGGTTTCCACAGATAA
                                                                                                                                                                                               Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. Feldmann, K. Full-Length cDNA from Arabidopsis thaliana
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Arabidopsis thaliana clone 256076 mRNA, complete sequence.
AY086529
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VCHRDLKPQNLLVDPLTHQVKICDFGSAKQLVKGEANISYICSRFYRAPELIFGATEY
TYZIDIWAGGCCLAELLLGQPLFPGRARNODQLVETIKVLGTPTREEIRCMNPHYTDFR
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PNGRPPPLENFKGEVAGSSPELVNKLIPDHIKRQLGLSFLNQSGT" /trānslation="MADDKEMPAAVVDGHDQVTGHIISTTIGGKNGEPKQTISYMAER VVGTGSFGIVFQAKCLETGETVAIKKVLQDRRYKNRELQLMRVMDHPNVVCLKHCFFS TTSKDELFLNLVMEYVPESLYRVLKHYSSANQRMPLVYVKLYMYQIFRGLAYIHNVAG ö 473 523 583 593 643 653 703 713 763 223 233 283 293 343 353 403 413 463 533 /product="shaggy-like protein kinase etha (EC 2.7.1.-)"
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VVGTGSFGI VFQAKCLETGETVAI KKVLQDRRYKNRELQLMRVMDHPNVVCLKHCFFS
TTSKDELFLNLVMEYVPESLYRVLKHYSSANQRMPLVYVKLYMYQI FRGLAYI HNVAG
VCHRDLKPQNLLVDPLTHQVK.CDFGSAKQLVKGRANISYI CSRFYRAPELI FCATTEY
TTSI DIWASAGCVLAELLLGQDLFPGENAVDQLVEI I KVLGTPTREEI RCMPHYTDFR
FPQI KMHPMHKI FHRWPPEALDFASHLLQYSPSLRCTALEACAHPFDEHREPNARL
PNGRPFPFLFFKQEVAGSSPELVNKLI PDHI KRQLGLSFLNQSGT"
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hote="abagy-like protein kinase etha"
hote="abart=1"
product="aT4g18710/F28A21_120"
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| brotein | ad="AAL77005.1"
| brotein | ad="AAL77005.1"
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The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H., Chenk, R., Kim, C.J., Meyersh, M.C., Banh, J. Bowser, L., Chang, E., Dale, J. M., Goldemith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Yamada, K., Yamamura, Y., Yang, C.C., Toriumi, M., Nu, H.C., and Ecker, J.R.
                                                                                                                                                                                                                             Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIS.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATCATTICCACTACTATAGGAGGCAAAAACGGCGAACCAAAGCAGACCATTAGTTACA
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Pred. No. 6.2e-166;
0; Mismatches 257;
                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RAFL02-10-D23(R21695)"
/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="compared to genome"
/replace="a"
                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 43.9%; al Similarity 77.1%; 863; Conservative
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Matches 863;
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Arabidopsis thaliana AT4g18710/F28A21_120 mRNA, complete cds.
AY075699
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Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J.,

Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D.,

Hayashizaki, Y., Ishida, J.; Jones, T., Kamiya, A., Karlin-Neumann, G.,

Kawai, J., Lae, J.M., Lin, J., Miranda, M., Narusaka, M.,

Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T.,

Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,

Theologis, A. and Ecker, J.R.

Gupublished
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCCGTTTTTCAATGAACTCCGAGAGCCAAACGCCCGTCTTCCAAATGGTCGTCCATTAC 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCGTTCTTTGATGAACTCAGAGAACCAAACGCTCGTTTACCAAATGGACGGCCTTTCC 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCCTCTCTTCAACTTCAAACAAGAAGTAGCTGGATCATCACCTGAACTGGTCAACAAGT 1253
                                 943
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-7AN-2002) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN arbaidopeis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Shinn, P., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T. Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
                                                         CATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCAC
                                                                                                                               CTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTAGGTTCCCACAAATCA
                                                                                                                                                                                                                                AAGCTCACCCTTGGCACAAGGTTTTTCATAAACGGATGCCTCCAGAAGCAATAGACCTTG
                                                                                                                                                                                                                                                               CATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACTGCGCTCGAAGCATGTGCTC
                               TTCCAGGAGAAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAATACCTGAGCATGTGAGACGACAAATGAGCACAGGATT 1283
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Arabidopsis thaliana
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LOCUS
DEFINITION
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KEYWORDS
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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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COMMENT

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URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi.S., Satoh.K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi.S., Satoh.K.,
Nagata.T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamco,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Rujimura,T., Kursumegi,T., Lu,M., Masada,H., Miura,J.,
Mizuno,K., Narikawa,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kursawa,R., Naikura,J., Oka,M., Xie,Q., Yokomizo,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Sugiyama,A., Harebaza,K. and Murskami,K.
Genome Exploration Research Group in Riken Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Pukuda,S., Hangaki,T.,
Haraoka,T., Hori,R., Iida,J., Imamura,K., Imotani,K., Ishi,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawa,J.J.,
Kishikawa-Hirozane,T., Watagawa,T., Muyazaki,J., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M.,
Ota,Y., Satoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Numasaka,R., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tagawa,A., Takahashi,F.,
Yasunishi,A., and Hayashizati,Y.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Le Johases I to 1863)

Adachi.J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Fujimura,T., Fukuda,S., Hanagaki,T., Hayashizaki,Y., Hayashizaki,Y., Hayashizaki,Y., Hayashizaki,Y., Hayashizaki,Y., Hayashizaki,Y., Hayashizaki,Y., Inda,Y., Ikeda,R., Imamura,K., Horta,I., Iida,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katch,H., Kawagashira,N., Kawai,J., Kayamata,M., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kodam,T., Kojima,Y., Murakami,Y., Matsubeai,T., Mizuno,H., Masuda,H., Matsubara,K., Matsuyama,T., Mizuno,H., Maxikawa,R., Mixura,J., Miyazaki,A., Mixuno,K., Murakami,K., Murakami,Y., Mixura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,M., Osato,N., Otano,Y., Sato,K., Satoh,H., Sakai,C., Sakai,C., Sakai,M., Shinagawa,A., Shiraki,T., Shishiki,T., Sagabe,Y., Sugano,S., Sugiawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Tamada,H., Yamada,H., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
                                                Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y. Collection, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences. Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skluchi@mias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-229-838-7007, Fax:81-229-838-7007, Fax:81-229-838-7007, Fax:81-229-838-7007, Fax:81-20-838-7007, Fax:81-20-8007, Fax:
Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                             Science 301 (5631), 376-379 (2003)
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J033086C10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 1863)
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PL CDNA, CAP trapper.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplanteae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Ehrhartoideae, Oryzeae, Oryza.
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TTEKDELFLALVMEYVPETLYRVLKHYSSANQMPLVYVKLYSYQI FRGLAYTHSCPG
VCHRDLKFQNILJVDDLTHQVKI CPFGSAKQLVKGEPNI SYI CSRFYRAPELI FGATEY
TTSI DI WASAGCVLAELLGQPL FPGENAVDQLVEI I KVLGTPTREER RCMNNYTDFK
FPQI KAHPWHKI FHRRMPPEN VDLASRILQYSPSIRCTALEACAHPFPDELREPNARL
PNGRPLPPLFFKQEVAGSSPELVNKLI PDHIKRQLGLSFLNQSGT"
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Direct Submission

Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud,
Institut de Biotechnologie des Plantes, Centre de Recharches sur
les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405
ORSAY Cedex, FRANCE
Corresponding genomic sequence is found in Y08947.
                                                                                                                                                                                                                                                                                                                               Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008) and X99696) (PGR97-008) and Y99696 (PGR97-008) and Y99696 (PGR97-008) and Y99601 and Y996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"

/kstrain="Columbia ecotype"
/db.xrei=txxon:3702"
/tisuue type="mix of several tissue types from different organs and developmental stages"
/clone_lib="Newman's lambda Zip Lox"
/dev stage="young shoots"
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                             1242 TCTTCTCAAGAGCTCATCAGCAGGCTCATACCAGAACATGTTCGACGGCAA
1219 GCTTCAATGGAGCTAATCAACAGGCTAATACCTGAGCATGTGAGACGACAA
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/db_xref="UniProt/Swiss-Prot:Q39011"
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/protein_id="CAA64109.1"
/db_xref="G1:1161512"
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                                                                                                             GAGGGAAATGACGCTGTTACTGGTCATATTCCACTACTATAGGAGGCAAAAACGGC
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                                                                   Gaps
                                                                1;
                      Length 1863;
                                                                Indels
                 Score 705.4; DB 8;
Pred. No. 4.4e-165;
0; Mismatches 221;
                 Query Match
Best Local Similarity 79.3%;
Matches 849; Conservative
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	AGACTGGAGAAACCGTGGCGATAAGAAGGTTTTGCCAAGATAGAAGATACAAGAACCGAG 441  AGTTGCAACTAATGCGACCAATGGATCACCCAAATGTCATCTCCTTGAAGCACTGTTTCT 463  AACTTCAGTTGATGCGTGGATGATCATCCCGAATGTGGTTTGTTGAAGCATTGCTTCT 501  TCTCTACAACGAGTAGATGATCATCCTCCAACTTATGGAGGATTGCTTCT 501  TCTCTACAACGAGTAGAACGATCTTCCTTCAACTTATGGAGTATGTACTGAGA 523  TTTCTACAACGAGAAAACGAATGTATTTCTTAAGAGTAATGTACTGAGA 523  TTTCTACAACAAGAAAAAAAAAAAAAAAAAAAAAAAAA			921 943 100 104 106	CATCTGGGTTCTTCAATATTCACCAAGTCTAGGCTGGGCCTCGAAGCATGTGCTC 1123  [
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\$ A &	8 8 8 8 8	6 6 6 6 6	6 6 6 6 6 6	8 6 8 6 8 6 8	8 4 8 4 8 4 8 4

Search completed: June 23, 2005, 21:28:41 Job time: 11292.4 secs

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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

June 23, 2005, 03:29:55; Search time 1265.83 Seconds (without alignments) 7547.973 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_16Dec04:\* 1: geneseqn1980s:\* Database

geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2004as: \* geneseqn2004bs: \* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2001as:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2001bs:\* genesegn1990s:\* genesegn2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

		Description	Aac42073 Arabidops	Aac47571 Arabidops	Aac37569 Arabidops		Aac47997 Arabidops	Abz13070 Arabidops	Adn73384 Thale cre	Aal54221 cDNA of w	Aac47206 Arabidops	Aah47004 Wheat gly	Abg82534 Wheat gly		Acc57973 Soybean p	Acc57970 Canola pr	Aac48014 Zea mays	Aac51694 Zea mays	Aac47761 Zea mays	Aac46604 Zea mays	Aac47763 Zea mays	Aac48306 Arabidops
SUMMAKIES		σr	AAC42073	AAC47571	AAC37569	ACC57975	AAC47997	AB213070	ADN73384	AAL54221	AAC47206	AAH47004	ABQ82534	AAC41916	ACC57973	ACC57970	AAC48014	AAC51694	AAC47761	AAC46604	AAC47763	AAC48306
		8	М	ო	٣	œ	m	ø	12	10	m	S	9	ო	80	æ	ო	m	m	m	m	٣
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	ouery	Match	96.9	59.1	58.9	47.3	44.2	44.0	44.0	44.0	44.0	43.5	43.5	43.3	43.0	42.1	41.7	41.3	37.6	36.3	35.8	35.6
		Score	1563.8	954.2	951	763.2	713.6	710.4	710.4	710.4	710.4	701.6	701.6	698.4	693.4	678.8	672.8	665.8	8.909	586	578	574
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06-MAY-1999; 06-MAY-1999;

Aac36960 Arabidops	Acc57962 Protein k		Aac45767 Arabidops	Add37156 Cell prol	. Add15740 Rice stre	Acc57977 Rice prot	Aah47001 Corn glyc	Abg82531 Maize gly		Adn72934 Thale cre	Acc57974 Soybean p	Aal55586 cDNA enco	Aac42818 Arabidops	Aah47003 Soy bean					Adg87959 A. thalia	Adn73136 Thale cre	Acc57961 Protein k	Acn53505 Cotton an	Adk66952 Gene #42	Aad11491 Human gly
AAC36960	ACC57962	ABZ14553	AAC45767	ADQ37156	ADQ15740	ACC57977	AAH47001	ABQ82531	AAC43095	ADN72934	ACC57974	AAL55586	AAC42818	AAH4 7003	ABQ82533	ACC57969	ACC57971	ABZ12869	ADG87959	ADN73136	ACC57961	ACN53505	ADK66952	AAD11491
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35.2	35.2	34.7	34.7	34.7	34.7	34.1	34.1	34.1	34.0	34.0	33.1	33.0	33.0	32.4	32.4	32.0	31.2	30.8	30.8	30.8	24.8	24.6	23.9	23.9
568	567.6	260	260	559.8	559.8	550	549.8	549.8	548.2	548.2	534	532.8	532.6	523.4	523.4	516.8	503	496.8	496.8	496.8	400	397.4	385.2	385.2
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Hybridisation assay, genetic mapping, gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss. Arabidopsis thaliana DNA fragment SEQ ID NO: 34186. AAC42073 standard; DNA; 1567 BP. 9905-0126264P. 9905-0126785P. 9905-0127462P. 9905-0128234P. 9905-0129845P. 9905-0130077P. 99US-0121825P. 99US-0123180P. 99US-0123548P. 99US-0125788P. 99US-0130449P. 99US-0130510P. 99US-0130891P. 99US-0132048P. 99US-0132407P. 99US-0132484P. 99US-0132485P. 99US-0132486P. 99US-0132487P. 25-FEB-2000; 2000EP-00301439 (first entry) Arabidopsis thaliana EP1033405-A2. 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 17-0CT-2000 06-SEP-2000. 25-FEB-1999; 16-APR-1999 23-APR-1999 28-APR-1999 08-APR-1999 05-MAY-1999 21-APR-1999 30-APR-1999 AAC42073; RESULT 1 AAC42073 

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11. MAY - 1999; 1998-01. 11. MAY - 1999; 1998-01. 14. MAY - 1999; 1998-01. 18. MAY - 1999; 1998-01. 20. MAY - 1999; 1998-01. 21. MAY - 1999; 1998-01. 22. MAY - 1999; 1998-01. 23. MAY - 1999; 1998-01. 24. MAY - 1999; 1998-01. 25. MAY - 1999; 1998-01. 26. MAY - 1999; 1998-01. 27. MAY - 1999; 1998-01. 28. MAY - 1999; 1998-01. 29. MAY - 1999; 1998-01. 20. MAY - 1999; 1998-01. 21. MAY - 1999; 1998-01. 22. MAY - 1999; 1998-01. 23. MAY - 1999; 1998-01. 24. MAY - 1999; 1998-01. 25. MAY - 1999; 1998-01. 26. MAY - 1999; 1998-01. 27. MAY - 1999; 1998-01. 28. MAY - 1999; 1998-01. 29. MAY - 1999; 1998-01. 21. MAY - 1999; 1998-01. 22. MAY - 1999; 1998-01. 23. MAY - 1999; 1998-01. 24. MAY - 1999; 1998-01. 25. MAY - 1999; 1998-01. 26. MAY - 1999; 1998-01. 27. MAY - 1999; 1998-01. 28. MAY - 1999; 1998-01. 29. MAY - 1999; 1998-01. 20. MAY - 1999; 1998-01. 21. MAY - 1999; 1998-01. 22. MAY - 1999; 1998-01. 23. MAY - 1999; 1998-01. 24. MAY - 1999; 1998-01. 25. MAY - 1999; 1998-01. 26. MAY - 1999; 1998-01. 27. MAY - 1999; 1998-01. 28. MAY - 1999; 1998-01. 29. MAY - 1999; 1998-01. 20. MAY - 1999; 1998-01. 20. MAY - 1999; 1998-01. 21. MAY - 1999; 1998-01. 22. MAY - 1999; 1998-01. 23. MAY - 1999; 1998-01. 24. MAY - 1999; 1998-01. 25. MAY - 1999; 1998-01. 26. MAY - 1999; 1998-01. 27. MAY - 1999; 1998-01. 28. MAY - 1999; 1998-01. 29. MAY - 1999; 1998-01. 20. MAY - 1999; 1998-01. 21. MAY - 1999; 1998-01. 22. MAY - 1999; 1998-01. 23. MAY - 1999; 1998-01. 24. MAY - 1999; 1998-01. 25. MAY - 1999; 1998-01. 26. MAY - 1999; 1998-01. 27. MAY - 1999; 1998-01. 28. MAY - 1999; 1998-01. 29. MAY - 1999; 1998-01. 20. MAY - 1999; 1998-01. 21. MAY - 1999; 1998-01. 22. MAY - 1999; 1998-01. 23. MAY - 1999; 1998-01. 24. MAY - 1999; 1998-01. 25. MAY - 1999; 1998-01. 26. MAY - 1999; 1998-01. 27. MAY - 1999; 1998-01. 28. MAY - 1999; 1998-01. 29. MAY - 1999; 1998-01. 20. MAY - 1999; 1998-01. 20. MAY - 1999; 1998-01. 21. MAY - 1999; 1998-01. 22. MAY - 1999; 1998-01. 23. MAY - 1999; 1998-			
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                 | TATGTACCTGAGACTTTATACCGGGTTTTGAGGCACTATACTACTACTTCTAATCAGAGGATG
                                     TATGTACCAGAGACATTGTACCGGGTTTTGAAGCACTATACTAGTTCAAACCAGCGGATG
                                                                                                                                                        ACTGTTCCCGGTGTTTGCCACAGAGTGTGAAACCACAAAATCTCTTGGTTGATCCCTTG
                                                                                                                                                                           ACTGCTCCTGGTGTCTGCCACAGAGATGTGAAACCACAAAATCTTTTGGTTGATCCCCTC
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                                                                                       CCAATITICIATGICAAGCITTACACATATCAAATCTITAGAGGITTGGCTTACATCCAT
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ive 0; Mismatches 170; Indels
99US - 0155659P.
99US - 0156458P.
99US - 0157117P.
99US - 015753P.
99US - 015763P.
99US - 015865P.
99US - 0158232P.
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                28 - SEF - 1999

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protein identification; signal transduction pathway; metabolic pathway;
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 ACATATCAAATCTTTAGAGGTTTGGCTTACATCCATACTGTTCCCGGTGTTTGCCACAGA
                                     <u> acararcaaarcirrasessarrascarararcaracescacressasrriscearass</u>
                                                                          GATGTGAAACCACAAAATCTCTTGGTTGATCCCTTGACCCATCAGGTTAAGCTGTGTAT
                                                                                                                                                     TITIGGAAGTGCAAAAGTATTGGTCAAAGGTGAACCAAACATATCATATATCTGCTCCCGT
                                                                                                                                                                                                                              TATTATCGTGCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCATAGATATA
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                                                                                                                                                                                                                                                                                                                       New protein kinase stress-related polypeptide coding nucleic acid, useful for producing transgenic plants with an increased tolerance to an environmental stress, e.g. high salinity, as compared to a wild type
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Pred. No. 3.3e-182;
0; Mismatches 254;
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9903-0159637P.
9903-0159638P.
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Matches 866; Conservative
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P-PSDB; ADN73385.
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                                                   The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell branacteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abloric stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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44.0%; Score 710.4; DB 6; Length 1143;
Best Local Similarity 77.1%; Pred. No. 2.1e-181;
Matches 864; Conservative 0; Mismatches 256; Indels 0;
                           Claim 144; SEQ ID NO 875; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                           Sequence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;
 increased tolerance
 producing plants with
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TTCCCGGAGAAATGCTGTGGATCAGCTCGTTGAAATTATAAAAGTTCTTGGTACACCAA
                                                                                                                                                                                                                                                                                                                                 CATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCACAGGCGCTCGAAGCTTGTGCAC
                                                                                                                                           CTCGAGAAAGAAATCCGTTGTATGAATCCACATTACACAGATTTCAGGTTTCCACAGATAA
                                                                                           CTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTAGGTTCCCACAAATCA
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growth regulator; animal feed product; thale cress;
cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
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1003
              or physiology, altered endoredupilcation, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/ or carbon metabolism or they function as transcription factors. This polynucleotide sequence is thale cress cDNA upregulated 1.3 fold or more in plants overexpressing the EZFA/DPA transcription factor, given in an exemplification of the invention.
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Pred. No. 2.1e-181;
0; Mismatches 256; Indels 0;
                                                                                                                                                                                                                                         Sequence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;
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Best Local Similarity 77.1%;
Matches 864; Conservative
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1021 ATCCGTTTTTCAATGAACTCCGAGAGCCAAACGCCCGTCTTCCAAATGGTCGTCCATTAC 1183 CGCCATTGTTCAATTTCAAACAAGAGTTAGGTGGAGCTTCAATGGAGCTAATCAACAGGC 1243 The invention relates to an isolated DWARF12 (DWF12) mutant polypeptide. The mutant polypeptide comprises at least 70 % sequence identity to the amino acid sequence of the DWF12 polypeptide given in the specification at positions 38-32 or 1-380, and having a mutation of at least one norconservative substitution, addition or deletion of an amino acid in a region of the polypeptide corresponding to a region given in the specification. The mutant DWF12 polypeptide is useful in producing transgenic plants that display at least one altered DWF12 phenotype, such as altered biochemistry, structure or morphology. The transgenic plant can be used in plant breeding or directly in agricultural production or 1004 AAGCTCACCCTTGGCACAAGGTTTTTCATAAACGGATGCCTCCAGAAGCAATAGACCTTG 1063 CATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACTGCGCTCGAAGCATGTGCTC 1123 ceccretericalerrealeagalerracides concarcine de contra d 901 961 DWARF12; DWF12; transgenic plant; plant breeding; industrial application; agricultural production; gene; ss. displaying altered biochemistry, structure or morphology which are useful in plant breeding, in agricultural production or industrial applications. New isolated DWARF12 mutant polypeptide for producing transgenic plants 842 AGGCACATCCCTGGCACAAGATCTTCCACAAAAGGATGCCCCCAGAAGCGTTGATTTTG CATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGTCAC /product= "Protein of wild-type DW12 locus" 1244 TAATACCTGAGCATGTGAGACGACAAATGAGCACAGGATT 1283 1082 rearrocaeaccararcaaeaeacaarreeercraaecrr 1121 Location/Qualifiers 200. 1312 /\*tag= a ВР (ARIZ-) ARIZONA BOARD OF REGENTS cDNA of wild-type DWF12 protein. Example 2; Fig 2; 62pp; English. AAL54221 standard; cDNA; 1490 15-MAY-2002; 2002WO-US015563 16-MAY-2001; 2001US-0291342P Tax F; P-PSDB; AA026726, AA026727. (first entry) Choe S, Feldmann K, WPI; 2003-129285/12 WO200292777-A2 Unidentified 27-MAR-2003 21-NOV-2002 1064 1124 1184 1022 AAL54221; 902 962 Key AAL5422 RESULT 셤 요 ઠે 셤 ð g ਨੇ g ⋩

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                                    ATCCGTTTTTCAATGAACTCCGAGAGCCAAACGCCCGTCTTCCAAATGGTCGTCCATTAC
                                                  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic
                                                                                                                           TAATACCTGAGCATGTGAGACGACAAATGAGCACAGGATT 1283
                                                                                                                                                 1281 rgarrccagaccararcaagagacaarrcggrcraagcrr 1320
                                                                                                                                                                                                                                                                              Arabidopsis thaliana DNA fragment SEQ ID NO: 52951
                                                                                                                                                                                                                                                                                                                           promoter; termination sequence; ss.
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990S-0130845P.
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16-APR-1999;
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07-MAY-1999;
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28-MAY-1999;
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industrial applications. The polynucleotide is useful in isolating or creating other mutant cell gene alleles, in inhibiting or enhancing endogenous DWF12 gene expression, and in standard diagnostic assays as hybridisation probe or primer. This polynucleotide sequence represents the cDNA of the wild-type DWF12 locus of the invention
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Score 710.4; DB 3;
Pred. No. 2.5e-181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein kinase; calcium-dependent phosphorylase kinase; CDPK; GSK-3; glycogen synthase kinase-3; GSK; ss.
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1058 ACCTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACTGCGCTCGAAGCAT 1117
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The present invention describes kinase polypeptides (I) such as a calcium dependent phosphorylase kinase polypeptide comprising a sequence of 101, 623, 157 or 111 (see ABP53632) amino acids, and a glycogen synthase kinase polypeptide comprising anino acids. and a glycogen comprising anino acids. (I) is something antibodies against the polypeptides, where the antibodies would be useful for immunological screening of CDNA expression libraries, and for preparing antibodies against the polypeptides, where the antibodies would be useful for detecting (I) in situ or in vitro, in cell extracts.

CC Nucleic acids (II) encoding (I) can be used to isolate CDNAs and genes encoding homologous proteins from the same or other plant species. (II) can a liso be used for creating transgenic plants in which (I) is present at higher or lower levels than normal or in cell types or in developmental stages in which they are not normally found. (II) are cuseful as probes or primers. The polynucleotides may be used as probes or primers. The polynucleotides may be used as probes or primers. The polynucleotides may be used as probes or primers. The polynucleotides may be used as probes or primers. The polynucleotides may be used as probes or brants for traits linked to those genes. The information can be used in plant breeding in order to develop lines with desired the prants of the used in plant breeding in order to develop.
                                                                                                                                                                                                                                                                                                synthase kinase; kinase; enzyme; plant; immunological screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New calcium-dependent phosphorylase kinase and glycogen synthase kinase polypeptides, for altering level of expression of kinase polypeptides in plants.
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                                                                                                                                                                                                                                                           Wheat glycogen synthase kinase encoding cDNA SEQ ID NO:15.
1238 ACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCAC 1277
                      1188 ACAGGCTTGTTCCGGAACATGTTCGACGGCAAAATGGCCC 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "glycogen synthase kinase"
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                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                        ABQ82534 standard; cDNA; 1673
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Score 701.6; DB 6; Pred. No. 5.9e-179; 0; Mismatches 299;

Query Match
Best Local Similarity 74.7%;
Matches 881; Conservative

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Length 1673;

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Hybridisation assay, genetic mapping, gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                          ACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCAC 1277
                                                                                                                         1188 Acadectretrecegaacaretregaedecaaaaredeee 1227
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The present sequence is a full-length cDNA encoding GmPK-1, a novel soybean protein kinase stress-related polypeptide (PKSRP). The cDNA was identified on the basis of homology to Physcomitrella patens PK-3 (see ACC57962) and PK-10 (see ACC57966) sequence. GmPK-1 is an example of PKSRPs of the invention that are important for modulating a plant's response to environmental stress. Over-expression of PKSRP coding nucleic acids in a plant results in the plant's increased tolerance to environmental stress. Transgenic monocot and dicot plants are provided that show increased tolerance to high salinity, drought and low
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transgenic plant; plant; stress tolerance; drought
salt tolerance; cold tolerance; soybean; gene; ss.
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The present sequence is a full-length cDNA encoding BnPK-2, a novel canola protein kinase stress-related polypeptide (PKSRP). The CDNA was identified on the basis of homology to Physcomitzella patens PK-3 (see ACC57962) and PK-10 (see ACC57966) sequence. BnFK-2 is an example of PKSRPB of the invention that are important for modulating a plant's response to environmental stress. Over-expression of PKSRP coding nucleic acids in a plant results in the plant's increased tolerance to environmental stress. Transgenic monocot and dicot plants are provided that show increased tolerance to high salinity, drought and low
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                PKSRP; enzyme;
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            protein kinase stress-related polypeptide; nic plant; plant; stress tolerance; drought
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                                                                                                                  cocation/Qualifiers
                                                                                                                                                                    /product= "BnPK-2"
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Canola protein kinase stress-related polypeptide BnPK-2 cDNA

(first entry)

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CGAGCTGTTTCTGAACTTGGTTATGGAGTATGTCCCTGAGAGCTTGTACCGAGTTCTGAA
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                 GCACTATACTAGTTCTAATCAGAGGATGCCAATTTTCTATGTCAAGCTTTACACATATCA
                              GATCTTCAGAGGACTTGCTTTCACATGTTGTTGCTGGAGTTTGTCACAGAGATCTAAA
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Query Match 41.7%; Score 672.8; DB 3; Best Local Similarity 75.7%; Pred. No. 3.6e-171; Matches 833; Conservative 0; Mismatches 267;

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15-SEP-1999;	0-SEP-199	-SEP-1	3-SEP-19	4-SEP-19	8-SEP-199	9-SEP-199	4-0CT-199	5-0CT-199	6-OCT-199	7-0CT-199	8-OCT-199	2-0CT-199	3-0CT-199	3-0CT-199	3-0CT-199	4-OCT-199	4-OCT-199	4-0CT-199	4-0CT-19	4-OCT-199	8-0CT-199	1-0CT-199	1-0CT-199	1-OCT-199	1-0CT-199	1-OCT-199	1-0CT-1	2-0CT-199	2-0CT-199	2-OCT-199	5-0CT-199	5-0CT-199	5-OCT-199	6-0CT-199	6-0CT-199	6-0CT-199	8-OCT-199	8-OCT-199	8-0CT-19	٦
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28 94.6 5.9 479 3 29 94.6 5.9 479 3 31 83.6 8.8 5.4 1544 2 31 83.6 8.8 5.0 1725 4 33 78.6 4.9 942 4 34 78.6 4.9 942 4 35 78.4 4.9 1467 1 36 78.4 4.9 1467 1 37 78.4 4.9 1467 2 38 78.4 4.9 1467 2 39 78.4 4.9 1467 3 41 78.4 4.9 1467 3 41 78.4 4.9 1467 3 41 78.4 4.9 1467 3 41 78.4 4.9 1467 3 41 78.4 4.9 1467 3 42 78.4 4.9 1467 3 43 78.4 4.9 1467 3 44 77.8 4.8 1041 4 44 77.8 4.8 1041 4 45 77.8 4.8 1041 4 45 77.8 4.8 1041 4 45 77.8 4.8 1041 4 46 77.8 4.8 1041 4 47 78.8 10.0000 5 PALENT INFORMATION: MOUNTER: 000000 5 PALENT INFORMATION: Erain COURRENT PILING DATE: 2000-05 7 CURRENT PELING DATE: 2000-05 7 CURRENT PILING DATE: 2000-05 7 CURRENT PROPARATION: CLOSE IN AUMBER: 9 7 SEQ ID NO 6 7 SEQ ID NO 6 7 CURRENT PILING DATE: 1998-05 7 CURRENT PROPAMATION: CLOSE IN AUMBER: 9 7 TITLE: from Arabidopsis thall 1 PAGES: 306-306 7 CURRENT PROPAMATION: (1.063) 7 CURRENT RESIDUES: (1)(163) 7 CURRENT PROPAMATION: (1000-100) 7 CURRENT PROPAM	US-08-461-018A-13 US-08-37-593-13 US-08-37-593-13 US-09-949-016-4276 US-09-671-050-11 US-09-671-050-5 US-08-176-620A-3 US-08-461-985-3 US-08-461-985-3 US-08-453-012C-3 US-08-932-778-3 US-08-932-778-3 US-08-932-778-3 US-08-932-778-3 US-08-932-778-3 US-08-932-778-3 US-08-932-778-3 US-08-932-778-3 US-08-932-778-3 US-08-932-012C-3 US-09-417-197-40 US-09-417-197-40 US-09-671-050-3	ht-SwS Storage Org Storage Org S78,194 a ecotype aves da ZAPII d -Dugue,N., SGG/GSK-3 ( Accession	Score 972.2; DB 4; Pred. No. 1.4e-281; 0; Mismatches 343; AAAGAG-TAAAAAAGCACATG                           TTTAGAGCTGTAAAAAAGCACATG CTTGCTCCGCCGCTGCAGCTT CTTGCTCCGCCGCTGCAGCTT
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0; Mismatches 299;
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Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Allen, Steve
TITLE OF INVENTION: Plant Protein Kinases
ITIE REPERENCE: BB-1171
CURRENT PILLING DATE: 1999-07-02
EARLIER PILING DATE: 1999-07-02
BARLIER PILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 15-07
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ORGANISM: Triticum aestivum
FEATURE:
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FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/654,731
CURRENT FILING DATE: 2001-05-14
FRIOR APPLICATION NUMBER: 60/092,438
PRIOR FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
LENGTH: 1673
                                                                                                                                                                TYPE: DNA ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 74.7
Matches 881; Conservative
                                                                                                                                                                                                                   ; NAME/KEY: unsure
; LOCATION: (1349)
US-09-854-731-15
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Patent No. 6794561
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
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US-09-854-731-15
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Patent No. 6794561
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT FILING DATE: 2001-05-14
FRIOR APPLICATION NUMBER: 60/092,438
FRIOR APPLICATION NUMBER: 60/092,438
FRIOR APPLICATION NUMBER: 60/092,438
FRIOR PILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 9
LENGTH: 1814
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CRGANISM: Zea mays
US-09-854-731-9
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Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Allen, Steve
TITLE OF INVENTION: Plant Protein Kinases
FILE REPRENCES: B8-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
BARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
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US-09-347-801-9
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US-09-347-801-9
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Pred. No. 1.2e-146;
0; Mismatches 313;
                                                                                                                                                                               APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
SEALIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 13
                                                                                                                            Sequence 13, Application US/09347801
Patent No. 6262345
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.4%;
Best Local Similarity 69.6%;
Matches 723; Conservative
TTCAATTTCAAAC
                   TYPE: DNA
ORGANISM: Glycine
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                                                                                                                                                                                         GTGACCAGCATTGATGGGAAATGGGCAAGCAAAGCAGACCATTAGTTACATGGCTGAG
                                                                                                                                                                                                                                                                CGGGTGGTAGGTCATGGGTCCTTCGGAACCGTTTTCCAGGCCAAGTGTCTTCAAACTGGT
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                                                       Gaps
             Score 549.8; DB 4; Length 1814;
Pred. No. 1.6e-154;
0; Mismatches 302; Indels . 0;
               34.1%;
             Query Match
Best Local Similarity 70.8
Matches 731; Conservative
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                                                                                                                                                                                                                                        Score 523.4; DB 4;
Pred. No. 1.2e-146;
0; Mismatches 313;
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al Similarity 69.6%;
723; Conservative
                                                (1297)
unsure
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unsure
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unsure
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                                                                                                                                                                                                                                        TGATTTTGGAAGTGCAAAAGTATTGGTCAAAGGTGAACCAAACATATCATATATCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                TATATGGTCTGCTGGTTGTGTACTGGCAGAGCTTCTTCTTGGCCCAGCCGTTATTTCCAGG
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CACTGAAAAGGATGAACTATACCTTAATTTGGTTCTCGAATATGTTCCTGAAACAGTTAA
                                                         591 TTACACATATCAAATCTTTAGAGGTTTGGCTTACATCCATACTGCTGTTCCCGGTGTTTGCCA
                                                                                                                                                                        CAGAGATGTGAAACCACAAAATCTCTTGGTTGATCCCTTGACCCCATCAGGTTAAGCTGTG
                                                                                                                                                                                                                                                                                                            771 CCGTTATTATCGTGCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCATAGA
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                                   CCGGGTTTTGAGGCACTATACTAGTTCTAATCAGAGGATGCCAATTTTCTATGTCAAGCT
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Patent No. 6794561
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/092,438
PRIOR RILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
LENGTH: 1429
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ORGANISM: Glycine m
PEATURE:
NAME/KEY: unsure
LOCATION: (1202)
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US-09-854-731-13
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                                                             637 GACTTTGGAAGTGCAAAGCAGCTGGTCCGAGGAGAACCCAATGTTTCGTATATCTGTTCT
                                                                                                                                                                                                   697 cegracraraecececedescricarcriresaeceaerearraraecereragar
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712 GATTTTGGAAGTGCAAAAGTATTGGTCAAAGGTGAACCAAACATATCTATATCTGCTCC
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Sequence 1414, Application US/09016434

Patent No. 6500938

GENERAL INPORATION:
APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Selhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS: ADDRESSES: ADDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERNCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/09/016,434
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APPLICATION NUMBER: US,
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCAATTTCA 1201
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STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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APPLICANT: Madeline M. Butler
APPLICANT: Robert McVay
APPLICANT: Robert McVay
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRES
CURRENT APPLICATION NUMBER: US/09/489,765A
CURRENT FILING DATE: 2000-01-19
                                                                                                                                                                      1130
                                                                                                                                                                                                                                           1183
                                                                 TCCATGGCACAAGATCTTCCATAAGGGCATGCCTCCAGAGGCTGTTGATTTGGTATCAAG 1123
                                                                                                                                                                                                                                                                                                                                                        ---TTTCAATGAACTCCGAGAGCCAAACGCCCGTCTTCCAAATGGTCGTCCATTACCGCC 1187
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                                                                                                                                                                                                              CCCTTGGCACAAGGTTTTTCATAAACGGATGCCTCCAGAAGCAATAGACCTTGCATCTCG
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65.5%; Pred. No. 4.4e-105;
ive 0; Mismatches 308; Indels 6;
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Best Local Similarity 65.54
Matches 596; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (40)...(1302)
US-09-489-765A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SEQ ID NO 3
LENGTH: 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-489-765A-3
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APPLICANT: Akihiko TAKASHIMA et al.
TITLE OF INVENTION: PREVENTYUE OR THERAPEUTIC AGENTS FOR
TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
WUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
1057 TTTGATGAATTACGGGACCCAAATGTCAAACATCCAAATGGGGGGGAACACACCTGCACT 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        800 TTGGAAATGGATCATTTGGTGGTATATCAAGCCAAACTTTGTGATTCAGGAGAACTGG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            860 İCGCCAICAAGAAAGIATIGCAGGACAAGAGATITAAGAATGGAGGCTCCAGATCATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 TAGCCATTAAAAAGGTCTTGCAAGATCGACGCTATAAAAACCGTGAGTTGCAACTAATGC
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Pred. No. 9.8e-105;
0; Mismatches 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
FILING DATE: February 20, 1996
CLASSIFICATION: 5.14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA to genomic RNA ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                  Sequence 1, Application US/08602264A Patent No. 5837853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
MEDIUM TYPE: 144
COMPUTER: IBM COMPATINE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 base pairs
TYPE: nucleic acid
STRANDEDNESS; double
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Best Local Similarity 65.6
Matches 594; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-602-264A-1
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                                                                                                                                                                                                                                                                                                  Score 385.2; DB 4;
Pred. No. 4.4e-105;
0; Mismatches 308;
                      INFORMATION FOR SEQ ID NO: 1414:
SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9529236
US-09-016-434-1414
                                                                                                                                                                                                                                                                                                  Query Match 23.9%;
Best Local Similarity 65.5%;
Matches 596; Conservative
     (650) 845-4166
     TELEFAX:
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                   US/08/461,018A
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA to genomic RNA
ORIGINAL SOURCE:
                                FILING DATE: June 5, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                 APPLICATION NUMBER: US/08/
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 base pairs
TYPE: muclète acid
STRANDEDNESS: double
   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   human being
                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM:
US-08-461-018A-1
                                                                                                                                                                                                           TELEPHONE
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                               476 GTAGAGATGAGCTCTTCCTCAACCTTGTTATGGAGTATGTACCTGAGACTTTATATACCGGG
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US-09-566-921-24
; Sequence 24, Application US/09566921
; Patent No. 666288
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
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US-09-216-958-1
; Sequence 1, Application US/09216958
; Patent No. 6248559
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK

STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                  1517 GGACTAAGGTCTTCCGACCCCGAACTCCACCGGAGGCAATTGCACTGTGTAGCCGTCTGC
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                     TTCGATGTATGAACCCCGAACTACACAGATTTTAGGTTCCCACAAATCAAAGCTCACCCTT
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,958
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA to genomic RNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,018
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
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; Sequence 3, Application US/09488856A; Patent No. 6316259; GENERAL INFORMATION:
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; LOCATION: (92)
US-09-488-856A-3
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US-09-488-856A-3
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TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE FILE REPREBNCE: PA-0024 US CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL PROGRAM
LENGTH: 1952
                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
ERATURE:
NAME/KEY: misc feature
OTHER INPORMATĪON: Incyte ID No. 6682888 234735.15
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Best Local Similarity 61.5%;
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APPLICANT: Brett P. Monia
APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Madeline Wyatt
APPLICANT: Jacqueline Wyatt
TITLB OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXPRIBERENCE: RTS-0115
CURRENT APPLICATION NUMBER: US/09/488,856A
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 88
LENGTH: 2154 1143 CCGAGAGCCAAACGCCCGTCTTCCAAATGGTCGTCCATTACCGCCATTGTTCAATTTCAA 1202 1108 GCGATGTCTGGGAACCCAGCTGCCTAACAACCGCCCACTTCCCCCTCTTCAACTTCAG 1167 1203 ACAAGAGTTAAGGTGGAGCTTCAATGGAGCTAATCAACAGGCTAATACCTGAGCATGTGAG 1262 988 GGTGTTCAAATCTCGAACGCCGCCAGAGGCCATCGCGCTCTGCTCTAGCCTGCTGGAGTA 1047 188 TGCTGGTGAACTCTCCATCCAACCGTCTCTCAACGCCATTCTCATCCCTCCTCACTTGAG 1227 771 471 365 425 591 542 602 662 531 651 711 246 AGGCAAAAACGGCGAACCAAAGCAGACCATTAGTTACATGGCTGAGCGGGTTGTTGGAAC 712 ccaciicaccaaggccaagrigaccaicciaircriciaigicaaggrgiacargiacca 412 AciccaAcecceAcAcecrcccAACAACAACTCCCTTACACCCACATCAAACTCATTCCCAA 306 AGGTTCATTCGGGGATTGTTTTTCAGGCGAAATGCTTGGAAAACTGGAGAATCAGTAGCCAT 472 recercatrioscorcereraceacecacecroseaceaceaceaceaceaceacea TAAAAAGGTCTTGCAAGATCGACGCTATAAAAACCGTGAGTTGCAACTAATGCGACCAAT ggaccacrecaararrergaggcreagaracrrrrrrrrrcracregegagaagaaga TGAGCTCTTCCTCAACCTTGTTATGGAGTATGTACCTGAGACTTTATACCGGGTTTTTGAG GCACTATACTAGTTCTAATCAGAGGATGCCAATTTTCTATGTCAAGCTTTACACATATCA 603 AATCTTTAGAGGTTTGGCTTACATCCATACTGTTCCCGGTGTTTGCCACAGAGATGTGAA 1083 TTCACCAAGTCTACGCTGCACTGCGCTCGAAGCATGTGCTCATCCGTTTTTCAATGAACT GGATCACCCAAATGTCATCTCCTTGAAGCACTGTTTCTTCTC---TACAACGAGTAGAGA Gaps 9 Length 2154; Ouery Match 23.3%; Score 375.8; DB 3; Best Local Similarity 61.5%; Pred. No. 3.9e-102; Matches 637; Conservative 0; Mismatches 392;

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Pred. No. 1.5e-101;
0; Mismatches 332;
                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRACTERISTICS:
LENGTH: 1972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: linear
MOLECULE TYPE: CDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: rat
                       FILING DATE: MATCH 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WATEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEPHONE:
TELEPA:
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Best Local Similarity 63.9%;
Matches 599; Conservative
APPLICATION NUMBER:
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US-08-602-264A-2

US-08-602-264A-2

Sequence 2, Application US/08602264A

FAPTHORMATION:
APPLICANT: Akihiko TAKASHIMA et al.
TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE

TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
COUNTRY: D.C.
COUNTRY: D.C.
REDIUM TYPE: DISEASE.
MEDIUM TYPE: DISEASE.
MEDIUM TYPE: DISEASE.
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                                       ACCACAAAATCTCTTGGTTGATCCCTTGACCCATCAGGTTAAGCTGTGTGATTTTTGGAAG
                                                                                                                                                                                       TGCAAAAGTATTGGTCAAAGGTGAACCAAACATATCATATATCTGCTCCCGTTATTATCG
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
PILING DATE: February 20, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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Search completed: June 24, 2005, 07:03:34 Job time : 395.175 secs



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GenCore version 5.1.6
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June.23, 2005, 10:41:47; Search time 1739.22 Seconds (without alignments) 5800.480 Million cell updates/sec Run on:

Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6067389 seqs, 3125258755 residues Searched:

12134778 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Database :

cgn2\_b/prodata/2/pubpna/PCT\_NEW\_PUB.csg:;
cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seg:;
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cgn2\_6/ptodata/2/pubpna/USOB\_PUBCOMB.seg:;
cgn2\_6/ptodata/2/pubpna/USOB\_PUBCOMB.seg:; /ptodata/2/pubpna/US07 PUBCOMB.seg: Applications NA:\* cgn2/

prodata/2/pubpna/US10D\_PUBCOMB.seq: prodata/2/pubpna/US10E\_PUBCOMB.seq: prodata/2/pubpna/US10F\_PUBCOMB.seq: ptodata/2/pubpna/US10G\_PUBCOMB.seg: prodata/2/pubpna/US10 NEW PUB.seq:\* /cgn2\_6/ptodata/2/pubpna/US11 NEW PUB.seq:\*/cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*/cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\* ptodata/2/pubpna/US10H ptodata/2/pubpna/US10I

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 6, Appli Sequence 25, Appl Sequence 98579, A Sequence 875, App Sequence 875, App Sequence 12, Appl Sequence 12, Appl
ΩΙ	21 US-10-764-138-6 16 US-10-292-408-25 19 US-10-437-963-98579 9 US-09-938-842A-875 21 US-10-477-687-12 18 US-10-425-114-12807
90	21 16 19 11 21 18
Length	1636 1744 1831 1143 1143 1726
Score	972.2 763.2 713.2 710.4 710.4 710.4
Result No.	0 11 2 18 4 18 18 1

	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	200044404666 40044464000 40080846000	1111277 9996, 67975, 29569, 5123, 24107, 9488, 81473,
US-10-424-599-67990 US-09-854-731-15 US-10-424-599-67987 US-10-424-599-67989 US-10-424-599-124786 US-10-424-599-124786 US-10-424-599-124786	10-425-115-2295 10-437-965-2987 10-437-965-2987 10-425-114-1745 10-425-115-3230 10-425-114-3299 10-425-115-3231 10-425-115-3231 10-425-115-3231	10-421-115-221 10-425-114-222 10-425-114-348 10-425-114-348 10-425-115-148 10-425-115-148 10-76-701-14-321 10-425-114-328	-10-425-115-1112 -10-437-963-9996 -10-425-114-2956 -10-739-930-5123 -10-739-408-2 -10-437-965-114-9488 -10-425-114-9488
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## ALIGNMENTS

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NAME/KEY: mRNA
LOCATION: (1). (1636)
OTHER INFORMATION: taxon:3702
OTHER INFORMATION: taxon:3702
OTHER INFORMATION: tissue type leaves
OTHER INFORMATION: tissue type leaves
OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots
PUBLICATION INFORMATION:
AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and Kreis, M.
TITLE: Three New DDNAS Related to SGG/GSK-3 ( Shaggy/Glycogen Synthase Kinase-3)
TITLE: from Arabidopsis thaliana ( Accession No. X94938, x94939 and X99696) ( PGR97-
I Instart
                                                                                                                                                             APPLICANT: Advanta Seeds B.V.
TITLE OF INVENTION: Modulation of Storage Organs
FILE REFERENCE: 026-106-10764,138
CURRENT FILING DATE: 2004-01-23
PRIOR PLING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PARENTE: 2000-05-24
NUMBER OF SEQ ID NOS: 6
SEQ ID NOS: 6
LENGTH: 1636
                                                      Sequence 6, Application US/10764138
Publication No. US20050081266A1
GENERAL INFORMATION:
APPLICANT: Sudwestdeutsche Saatzucht-SWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Arabidopsis sp.
                            US-10-764-138-6
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1050

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1170 1148 1268

1328 1391 1388 1451

1511

METHODS

x99696.rnpb

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969 TTCCCACAAATCAAAGCCCACCTTGGCATAAGGTTTTCCACAAGCGGATGCCTCCGGAA 1028
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                                          CITGGIACICCAACICGIGAAGAAAIICGAIGIAIGAACCCGGAACIACACAGAIIIIAAGG
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; Publication No. US20030182692A1
; GENERAL INFORMATION:
    APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, RUCYING
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METH
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METH
; TITLE OF INVENTION: OF USE IN PLANTS
; TITLE OF INVENTION: 0.0 USE IN PLANTS
; FILE REFERENCE: 16313-0178
; CURRENT APPLICATION NUMBER: US/10/292, 408
; CURRENT PILING DATE: 2002-11-12
; PRIOR FILING DATE: 2001-11-09
; NOWHER OF SEC ID NOS: 51
; SEQ ID NO 25
; LENGTH: 1744

TUBE OF THE                                                                 CTTGGTACTCCAACTCGCGAAGAATCCGGTGCATGAACCCAAACTACACAGACTTCAGA
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ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                      Length 1636;
                                                                                                                                                                                                                                      Query Match
60.2%; Score 972.2; DB 21; Length
Best Local Similarity 77.0%; Pred. No. 6.3e-260;
Matches 1234; Conservative 0; Mismatches 343; Indels
               JOURNAL: Plant Physiol.

VOLUME: 113

ISSUE: 1

PAGES: 306-306

DATE: 1997-01-01

DATABASE ACCESSION NUMBER: genbank/X94938

DATABASE ENTRY DATE: 1998-02-13

RELEVANT RESIDUES: (1)..(1636)

US-10-764-138-6
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US-10-437-963-98579
                                                                       CATGTGAGACGACAAATGAG 1274
                                                                                         Caratragggggggarggg 1271
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ORGANISM: Oryza sativa
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US-10-437-963-98579/c
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   Length 1744;
  Score 763.2; DB 16; Length
Pred. No. 1.3e-201;
0; Mismatches 248; Indels
  47.3%;
Query Match 47.3
Best Local Similarity 78.6
Matches 912; Conservative
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Sequence 98579, Application US/10437963
; Sequence 98579, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: David K.
; APPLICANT: David K.
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; APPLICANT: David K.
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT PRIJING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 98579
; LENGTH: 1831 1135 AATGAACTCCGGAGAGCCAAACGCCCGTCTTCCAAATGGTCGTCCATTACCGCCATTGTTC 1194
1132 GATGAGCTTCGCGAACCAAATGCCCGGCTACCTAATGGCCGTCCACTGTTC 1191 1195. AATTTCAAACAAGAGTTAGGTGGAGCTTCAATGGAGCTAATCAACAGGCTAATACCTGAG 1254
1192. AACTTCAAACAGGAGTTAGCTGGAGCATCACCTGAACTGATCAATAGGCTCATCCAGAG 1251 1532 1472 1412 1352 ö 267 327 387 447 507 1531 CGGACAATTAGTTATATGGCGGAGCGAGTTGTAGGAACTGGTTCTTTCGGGATTGTTCTT 1471 CAGGCTAAGTGCTTGGAGACGGGGGAAACGGTGGCCATCAAGAAGGTGTTGCAGGACCGG CGTTACAAGAACCGTGAACTGCAGCTTATGCGCGCAATGGAACACCCCCAATGTCATCTCGC 448 TTGAAGCACTGTTTCTTCTCTACAACGAGTAGAGATGAGCTCTTCCTCAACCTTGTTATG GACGCTGTTACTGGTCATATCATTTCCACTACTATAGGAGGCAAAAACGGCGAACCAAAG CAGACCATTAGTTACATGGCTGAGCGGGTTGTTGGAACAGGTTCATTCGGGATTGTTTTT CAGGCGAAATGCTTGGAAACTGGAGAATCAGTAGCCATTAAAAAGGTCTTGCAAGATCGA CGCTATAAAAACCGTGAGTTGCAACTAATGCGACCAATGGGATCACCCAAATGTCATCTCC Gaps Length 1831; ö

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APPLICANT: Harper, Joef
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
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APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
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Best Local Similarity
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                                               542 AAATCTGTGACTTTGGCAGTGCGAAACAGCTCGTTAAAGGTGAAGCCAACATTTCTTACA
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44.0%; Score 710.4; DB 21; Length 1490;
Best Local Similarity 77.1%; Pred. No. 6.3e-187;
Matches 864; Conservative 0; Mismatches 256; Indels 0;
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JAPPLICANT: Tax, Frans
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JAPPLICANT: Tax, Frans
JAPPLICANTION: DWF12 and Mutants Thereof
FILE REFERENCE: 11696-075031
JUNEARY FAPLICATION NUMBER: US/10/477,687
CURRENT APPLICATION NUMBER: PCT/US02/15563
PRIOR PILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US 60/291,342
PRIOR PILING DATE: 2001-05-16
JENGTH: 1490
SEQ ID NO 12
LENGTH: 1490
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US-09-938-842A-875

i Sequence 875, Application US/09938842A

sequence 876, Application US/09938842A

sequence 876, Application US/09938842A

i Publication No. US20040009476A9

i GENERAL INFORMATION:

i APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: SANE, AND WETHODS OF USE

TITLE OF INVENTION: SANE, AND WETHODS OF USE

TITLE OF INVENTION: SANE, AND WETHODS OF USE

TITLE OF INVENTION: SANE, AND WETHODS OF USE

FILE REFERENCE: SCRIPII300-3

CURRENT PILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: S379

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Pred. No. 5.4e-187;
0; Mismatches 256; Indels 0;
                          TAATACCTGAGCATGTGAGACGACAAATGAGCACAGGATT 1283
                                                                    1082 TGATTCCAGACCATATCAAGAGACAATTGGGTCTAAGCTT 1121
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-875
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Best Local Similarity 77.1%;
Matches 864; Conservative
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RESULT 7

US-10-425-114-12807

US-10-425-114-12807

SQUENCE 12807, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Streen, Streen, Streen, Streen, Streen, Streen, Streen, Streen Streen, Streen Streen, Streen Streen, Streen Streen, Streen Streen, Streen Streen, Streen Streen, Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen Streen
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Pred. No. 1e-185;
0; Mismatches 273; Indels 0;
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US-10-425-114-12807
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Best Local Similarity 76.1%;
Matches 870; Conservative
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LENGTH: 1726
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190 ACTTCTTTGGGCCAGCCATTATTCCCTGGCGAAAATGCAGTAGACCAGCTTGTACATAT
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                                          TGGCGCCACAGAGTATACAGCATCCATAGATATATGGTCTGCTGGTTGTGTACTGGCAGA
AGGTGAAGCTAATATATCATACATATGTTCACGATTCTATCGAGCACCAGAACTTATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Clone ID: PAT_MRT3847_32408C.1
US-10-424-599-67990
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Matches 870; Conservative
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US-10-424-599-67990
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Sequence 67987, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
BAPLICANT: La Rosa Thomas J
APPLICANT: Chou Yihua
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER: OF SEQ ID NOS: 285684
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Pred. No. 6.5e-184;
0; Mismatches 277;
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Best Local Similarity 75.8%;
Matches 866; Conservative
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                                                                                                                                                                                APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TILLE OF INVENTION: Plant Protein Kinases;
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT APPLICATION NUMBER: 60/092,438
FILOR FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 15
                                                                                    ; Sequence 15, Application US/09854731; Patent No. US20020120949A1; GENERAL INFORMATION:
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With Associated 302 182 242 343 403 362 463 422 542 643 283 523 482 583 602 703 662 763 722 823 782 883 CTTTATACCGGGTTTTGAGGCACTATACTAGTTCTAATCAGAGGATGCCAATTTTCTATG 123 rescricaciara acida reference en caracide carica en caracteriste en construir en caracteriste en construir en caracteriste ACATCATATCTACAACTATTGGAGGCAAAATGGGGGAACCCAAACAGACTATTAGTTACA TGGCTGAGCGGGTTGTTGGAACAGGTTCATTCGGGAATTGTTTTTCAGGCGAAATGCTTGG rescricia e cestrar esta con contra contra en c AAACTGGAGAATCAGTAGCCATTAAAAAGGTCTTGCAAGATCGACGCTATAAAAACCGTG AGTIGCAACTAATGCGACCAATGGATCACCCAAATGTCATCTCCTTGAAGCACTGTTTCT TCTCTACAACGAGTAGAGATGAGCTCTTCCTCAACCTTGTTATGGAGTATGTACCTGAGA TTTCAACTACAAGTACAGATGAGCTTTTTCTTAATTTGGTGATGGAATATGTTCCAGAGT ccargranagagrantaagcacranacraargcraarcaagaargccaarcarcrarg 543 raaaacriracargraccagarrircagggarriggcrirararccacacrigricccaaag TITGCCACAGAGATGTGAAACCACAAAATCTCTTGGTTGATCCCTTGACCCATCAGGTTA AGCTGTGTGATTTTGGAAGTGCAAAAGTATTGGTCAAAGGTGAACCAAACATATA TATGTTCACGATTCTATCGCGCTCCAGAACTTATATTTGGCGCCACAGAGTATACAAGTT 224 ATATCATTTCCACTACTATAGGAGGCAAAAACGGCGAACCAAAGCAGACCATTAGTTACA TCAAGCTTTACACATATCAAATCTTTAGAGGTTTGGCTTACATCCATACTGTTCCCGGTG TTTGCCACAGAGACTTGAAAGCCTCAAAATATACTGGTGGATCCTCTTACACACCAAGTGA CCATAGATATATGGTCTGCTGGTTGTACTGGCAGGCTTCTTCTTGGCCAGCCGTTAT Gape APPLICANT: La CONTILLON TO A APPLICANT: Kovalic David K APPLICANT: Xovalic David K APPLICANT: Xovalic David K APPLICANT: Zhou Yihua APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(3322)B CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SEQ ID NO 67989 Length 1744; 1; TGGATTCTGATAAGGAAATGTCTGCAGCTGTTATTGAGGGAAATGACGCT Score 699.2; DB 18; Length Pred. No. 9.2e-184; 0; Mismatches 248; Indels ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_32407C.1 US-10-424-599-67989 Sequence 67989, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION: Query Match
Best Local Similarity 77.5%;
Matches 859; Conservative TYPE: DNA ORGANISM: Glycine max ઠ 셤

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Sequence 21, Application US/10292408

Publication No. US20030182692A1

GENERAL INFORMATION:
APPLICANY: VAN THIELEN, NOCHA
APPLICANY: DA COSTA E SILVA, OSWALDO
APPLICANY: CHEN, RUOYING
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICANTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 124786
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                                   843 TTCCTGGCG-AAATGCAGTAGAACCAGCTTGGTCATATTATAAAGGTGCTTGGCACACCCA
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TICCAGGAGAAATICAGIIGAICAGCIIGIGGAGAICAIAAAGGIICTIGGIACTICCAA
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US-10-424-599-124786
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Best Local Similarity
Matches 892; Conserva
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US-10-424-599-124786
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TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS TITLE OF INVENTION: OF USE IN PLANTS FILE REPERENCE: 16313-0178
CURRENT APPLICATION NUMBER: US/10/292,408
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/346,096
PRIOR PILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 21
                                                                                                                                                                                                                                                      GCGGCTCCGACGCCGGCACGAAAAGGAAATGTCAGCTCCTGTCGCAGATGGTAGATG
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Pred. No. 3.5e-182;
0; Mismatches 266; Indels
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Best Local Similarity 76.2%;
Matches 853; Conservative
                                                                                                                                     ; TYPE: DNA
; ORGANISM: Glycine max
US-10-292-408-21
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With Sequence 26109, Application US/10424599

Sequence 26109, Application US/2040031072A1

Sequence 26109, Application No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: La Rovalic David K

APPLICANT: APPLICANT: And Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated V

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NOS: 285684 1052 CAATAGACCTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCGCTCG 1111
1053 CAATTGACCTTGCATCAAGGCTTCTCCAATATTCCCCAAAACTTCGTTACAGTGCAGTGG 1112 1172 GTCGTCCATTACCGCCATTGTTCAATTTCAAACAAGAGTTAGGTGGAGCTTCAATGGAGC 1231 1173 GTCGTCCACTGCCTCCACTTTTCAACTTTAAACAGGAATTAGATGGAGCGCCCCCTGAAC 1232 AAGCATGTGCTCATCCGTTTTTCAATGAACTCCGAGAGCCAAACGCCCGTCTTCCAAATG 1171 ö 273 211 271 333 331 393 391 453 451 513 511 573 933 TIGGCACTCCTACTCGAGAAGAAATTCGATGCATGAATCCTAATTATACAGATTTCAGAT TCCCCCATATCAAAGCTCATCCTTGGCATAAGGTTTTTCACAAGCGAATGCCTCCTGAAG CTGTTACTGGTCATATCATTTCCACTACTATAGGAGGCAAAAAACGGCGAACCAAAGCAGA 954 ACAAAAATCGTGAACTGCAGTTAATGCGGTGATGGATCACCCAAATATAATTTCCTTGA 152 GCCGTCCTGAATTGGATTCTGATAAGGAAATGTCTGCAGCTGTTATTGAGGGAAATGACG 214 GCGCCCCGACGCCGCACGAAAAGGAAATGTCAGCTCCTGTCGCAGATGGTAATGATG 274 CACTCACTGGTCACATAATCTCAACCACAATTGCAGGCAAAAATGGCGAACCTAAACAAA 334 CCATCAGTTACATGGCCGAACGTGTTGTTGGCACTGGATCATTTGGCATTGTTTTCCAGG AGCACTGTTTCTTCTCTACAACGAGTAGAGATGAGCTCTTCCTCCAACCTTGTTATGGAGT TCCCACAAATCAAAGCTCACCCTTGGCACAAGGTTTTTCATAAACGGATGCCTCCAGAAG CCATTAGTTACATGCTGAGCGGGTTGTTGGAACAGGTTCATTCGGGATTGTTTTCAGG CGAAATGCTTGGAAACTGGAGAATCAGTAGCCATTAAAAAGGTCTTGCAAGATCGACGCT ATAAAAACCGTGAGTTGCAACTAATGCGACCAATGGATCACCCCAAATGTCATCTCCTTGA Gapa ö Length 1553; Query Match 43.0%; Score 693.4; DB 18; Length Best Local Similarity 76.2%; Pred. No. 3.6e-182; Matches 853; Conservative 0; Mismatches 266; Indels TAATCAACAGGCTAATACCTGAGCATGTGAGACGACAAA 1270 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_123578C.1 US-10-424-599-26109 TYPE: DNA ORGANISM: Glycine max LENGTH: 1553 1112 1233 212 394 ( 392 1172 1232 272

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US-10-455-115-22950/C

SUBJICATION NO. US20040214272A1

SUBJICATION NO. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REPERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 22950
                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Zea mays
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                                                                         Length 1779;
                                                                       Score 684; DB 20; Length 1
Pred. No. 1.6e-179;
0; Mismatches 250; Indels
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_120933C.1
US-10-425-115-22950
                                                                           42.48;
                                                                                                                 834; Conservative
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Best Local Similarity
Matches 834; Conserv
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Search completed: June 24, 2005, 08:33:20 Job time : 1743.22 secs



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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June 23, 2005, 10:16:02; Search time 8015.32 Seconds (without alignments) 7664.793 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

34239544 seqs, 19032134700 residues Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST: \* Database :

gb\_est1:\*
gb\_est2:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES Re

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Score	1293.2	1284.6	713.2	919	. 665	635.4	603.4	584.4	581.8	576.6	575	574	572.2	572	551.4	551.2	549.2	547.4	547	540.6	536	533.4	532	529
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528.8	526	524.2	521.6	515.2	513	511.8	508	505	503.4	502.2	501	500.4	494.8	494.6	491.6	491.2	491	488	486.4	485.4
25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

CNSOABIV 1461 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone	GSLTSIL422C04 of Silique of Strain col-0 of Arabidopsis thaliana (thale gress).	EAST 1000.1 GT: 42471112	Arabidopsia (thale cress)	Arabidopata thallana Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,	Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple G. Caboche M. Weigsenhach J. and Salanoubat.M.	Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:	A Combined Approach to Evaluate and Improve Arabidopsis Genome	Annotation	Unpublished	2 (bases 1 to 1461)	Genoscope.	Direct Submission	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr	- Web : www.genoscope.cns.fr)	The sequences are based on single pass reads.	LITE TECHNOLOGIES (a division of invitrogen) members carried out full-length librairies construction : Temple G.	Genoscope members carried out sequencing and annotation : Castelli	V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,	Schachter V., Weissenbach J., Salanoubat M.	URGV INRA : Clepet C., Caboche M.	Annotation is based on the June 2003 version of the Arabidopsis	genome released by MIPS (Munich Information center for Protein	Sequences). 5 prime and 3 prime are assembled with Phrap.	http://www.genoscope.cns.ir/externe/sequences/Banque_Frojet_Er/Full	tength
RESULT 1 CNSOAB1V LOCUS DEFINITION	NOTOGEOGR	VERSION	SOURCE	ORGANISM	\$CNG GGG GG	AUTHORS		TITLE			JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL		COMMENT										

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis. Location/Qualifiers Location/Qualifiers 1. .1461 /organism="Arabidopsis thaliana" /mol\_type="RNA" /strain="Col-0" /db\_xref="taxon:3702"

FEATURES

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                                                                              DB 3; Length 1461,
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                                                                            Score 1293.2;
Pred. No. 0;
0; Mismatches
/tissue type="Silique"
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1..1461
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Best Local Similarity 99.8%;
Matches 1295; Conservative
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CNSOABET

Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSITLSI12G09 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).

BX815323.1 G1:42471412

BX815323.2 G1:42471412

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Embryophyta; Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M. Temple,G., Caboche,M., Weissenbach,J., and Salanoubat,M. Anotherica Approach to Evaluate and Improve Arabidopsis Genome
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The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. length, http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full length
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
901 ACTCCAACTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTAGGTTCCCA 960
                                                                                 CAAATCAAAGCTCACCCTTGGCACAAGGTTTTTCATAAACGGATGCCTCCAGAAGCAATA
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Location/Qualifiers
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

Ehrhartoideae; Oryzeae; Oryza.

Enrhartoideae; Oryzeae; Oryza.

Ma.L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
An analyysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
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/clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
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Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
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Rice genomic sequence.
Class: exon-trapped.
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                                                                                                                                                      Score 1284.6;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.7%;
Matches 1287; Conservative
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Submitted (25-ARP-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA Missouri, Columbia, MO 65211, USA treested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.radb.iastate.edu, TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 17%)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

Maize Mapping Project/DuPont Consensus Sequences for Design of
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/mol_type="mRNA"
/mol_tref="mRNA"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
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Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones, these are publicity available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of t maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, lowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

Location/Qualifiers
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/lab_host="DH10B-TonA"
/clone lib="potato abiotic stress cDNA library"
/clone lib="potato abiotic stress cDNA library"
/note="Vector: pCWNSport6.1; Site_1: ECORI; Site_2: NotI;
supplier: Solamum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
c for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CK266410 924 bp mRNA linear EST 03-AUG-2004 EST712488 potato abiotic stress CDNA library Solanum tuberosum cDNA clone POAC457 5' end, mRNA sequence.
                                                                                     ATGCCTCCTGAAGCCATTGACCTTGCTTCTCTTCCATTCACTATTCACCAAGTCTTCGC 1159
                                                                                                                                                                                                                                                                                                                        TGCACTGCGCTCGAAGCATGTGCTCATCCGTTTTTCAATGAACTCCGAGAGCCAAAACGCC 1158
                                                                                                                                                                                                                                                                                                                                                  CGTCTTCCAAATGGTCGTCCATTACCGCCATTGTTCAATTTCAAACAAGAGTTAGGTGGA 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTTCAATGGAGCTAATCAACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCACA 1278
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
I (bases I to 924)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2003)

Contact: Robin Buell

The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/.
Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAGATITITAGGITCCCACAAATCAAAGCTCACCCTTGGCACAAGGITTTTCATAAACGG
                                                                                                                                                                                                                                      ATGCCTCCAGAAGCAATAGACCTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db xref="taxon:4113"
clone="POAC457"
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/cultivar="Kennebec"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1279 GGATTACAAAACAGTTA 1295
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CK266410.1 GI:39823388
                                                                                                                                                                                                                                                                            1100
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6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ö 240 607 300 667 360 727 427 120 487 180 547 9 1 GGTCCTTTGGGATAGTGTTTCAGGCAAAATGCCTTGGAAACTGGAGAGACTGTGGCCATAA 368 AAAAGGICTIGCAAGAICGACGCIAIAAAAACCGIGAGTIGCAACIAAIGCGACCAAIGG 428 ATCACCCAAATGTCATCTCCTTGAAGCACTGTTTCTTCTTCTACAACGAGTAGAGATGAGC ATACTAGTTCTAATCAGAGGATGCCAATTTTCTATGTCAAGCTTTACACATATCAAATCT 241 ATAGCAATTCAAATCAAAGGATGCCACTCATATATGTCAAACTTTACATGTATCAGAATA 301 TCAGAGGGCTGGCTTACATTCATAATGTTCCAAGAATTTGCCATAGAGATGTGAAACCTC 308 GITCATTCGGGATTGTTTTTCAGGCGAAATGCTTGGAAACTGGAGAATCAGTAGCCATTA TTAGAGGTTTGGCTTACATCCATACTGTTCCCGGTGTTTGCCACAGAGATGTGAAACCAC AAAATCTCTTGGTTGATCCCTTGACCCATCAGGTTAAGCTGTGTGATTTTGGAAGTGCAA 488 TCTTCCTCAACCTTGTTATGGAGTATGTACCTGAGACTTTATACCGGGTTTTGAGGCACT Gaps ö Length 924; Indels Score 635.4; DB 7; Pred. No. 3.3e-154; 0; Mismatches 176; Query Match 39.4%; Best Local Similarity 80.8%; Matches 741; Conservative (

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420 787 480 847 540 907 909 967 1087

333 300

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Submitted (25-ARR-2002) Maize Mapping Project, University of Submitted (25-ARR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.lastate.edu; TIGR, www.ingr.org; or NCBI, www.ncbi.nlm.nln.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.lastate.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTC 16-OCT-2002
                                                                                                                                             361 AAAAACCGTGAGTTGCAACTAATGCGACCAATGGATCACCCAAATGTCATCTCCTTGAAG 420
                                                                                                                      GTTACTGGTCATATCATTTCCACTACTATAGGAGGAAAAACGGCGAACCAAAGCAGACC 273
                                                                                                                                                                                                                                                                                                                        301 AAATGCTTGGAAACTGGAGAATCAGTAGCCATTAAAAAGGTCTTGCAAGATCGACGCTAT 360
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
CCTCAGCCTCATGCTCCTTGCTCCGCCGCTGCAGCTTCACGACGGCGACGCTTTGAAACGC 120
                                     CGTCCTGAATTGGATTCTGATAAGGAAATGTCTGCAGCTGTTATTGAGGGAAATGACGCT
                                                                                                                                                                                                                               241 ATTAGTTACATGGCTCAGCGGGTTGTTGGAACAGGTTCATTCGGGATTGTTTTTCAGGCG
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                                                                                                                                                                                                                                                                                                                                                                  AAAAACCGTGAGTTGCAACTAATGCGACCAATGGATCACCCAAATGTCATCTCCTTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTGTTTCTTCTTCTACAACGAGTAGAGATGAGCTCTTCCTCCAACCTTGTTATGGAGTAT
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26a mays PCO153236 mRNA sequence.
AY103545
AY103545.1 GI:21206623
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/mol_type="mRNA"
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Unpublished (2002)
2 (bases 1 to 1967)
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                                                                                                                                                                                                                                                                                                                        AV827407
AV827407 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-15-A20 5',
                                                                                                AGCCAAACGCCCGTCTTCCAAATGGTCGTCCATTACCGCCATTGTTCAAATTTCAAACAAG 1207
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Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
                                                           840
                                                                                                                   Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/lab host="BAPIDs"
/clone_lib="RAFL9"
/note="Site 1: BamH1; Site 2: Sal1; subjected to dehydration"(1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, hr) treatments"
                CAAGTCTACGCTGCACTGCGCTCGAAGCATGTGCTCATCCGTTTTTCAATGAACTCCGAG
                                        ATTGTTCAGTGGTTGAGAGAGAAAGAGTAAAAAAGCACATGGCCTCATTACCATTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 ATTGTTCAGTGGTTGAGAGAAAAGAGTAAAAAAGCACATGGCCTCATTACCATTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
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|mol_type="mRNA"
|db_xref="taxon:3702"
|clone="RAFL09-15-A20"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                      AGTTAACTGGAGCTTCA
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615; Conservative
                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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1357 1130 1417 1190 1477

EST 23-SEP-2004

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Asparagus officinalis (garden asparagus)
Asparagus officinalis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
Asparagaceae; Asparagus.
1 (bases 1 to 932)
dePamphilis,C., Carlson,J., Ma,H., Soltis,D., Soltis,P.,
CCCATGGCACAAGGTATTCCACAAAAGGATGCCGCCAGAAAGCTGTTGATCTGGTCTTCG
                                                                                                                                                                     1418 CTTTGATGAGCTTCGAGATCCTAATACTCGCCTTCCAAATGGTCGCTTTTTGCCACCACT
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                                                          GCTTCTTCAATATTCACCAAGTCTACGCTGCACTGCGCTCGAAGCATGTGCTCATCCGTT
                                                                                             1358 GCTACTCCAGTACTCCCCAAATCTGAGATGCACTGCTATGGAGGCACTTGTTCACCCATT
                                                                                                                                 1131 TTTCAATGAACTCCGAGAGCCAAACGCCCGTCTTCCAAATGGTCGTCCATTACCGCCATT
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aof01-15ms3-g01 Aof01 Asparagus officinalis cDNA clone
aof01-15ms3-g01 5', mRNA sequence.
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Contact: Claude dePamphilis or James Leebens-Mack
Mueller Laboratory
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Pred. No. 3.1e-140;
0; Mismatches 217;
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CV290871.1 GI:52576601
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                                                            /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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Pred. No. 7.6e-141;
0; Mismatches 281;
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208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
TTel: 814 865 9131
Eax: 814 865 9131
Email: cwd3@psu.edu or jhll0@psu.edu
The sequence provided is trimmed of vector and low quality regions.
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: aof01-15ms3 row: g column: 01 237 178 GAAATGTCTGCAGCTGTTATTGAGGGAAATGACGCTGTTACTGGTCATATCATTTCCACT Gaps .. 0 Length 932;

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                                         ACTATAGGAGGCAAAAACGGCGAACCAAAGCAGACCATTAGTTACATGGCTGAGCGGGTT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehthartoideae; Oryzeae; Oryza
1 (bases 1 to 2255)
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/organism="Oryza sativa (indica cultivar-group)

/mol type="genomic DNA"

/do Arref="texon:39946"

/clone lib="Oryza sativa Express Library"

/note="Oryza sativa exon trapped genomic sequen
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llarity 76.0%; Pred. No. 8.5e-139;
Conservative 0; Mismatches 224;
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/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone=lb="wiscotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCWVSport6.1; Site 1: ECoR1; Site 2: Not1;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Fseudomonas syringae py tomato 12 hr;
Xanthomonas campestris py campestris 12 hr, 18hr;
Pseudomonas syringae py phaseolicola 18hr, and Xanthomonas
campestris py vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 910)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
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                       776
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897 GAATCCCAATTACACAGAATTTCAAATTTCCGCAGATAAAAGCATGCCCATGCCATGCCACAAGT
                                                                                                                                                                                                                                                                                           TTTTCATAAACGGATGCCTCCAGAAGCAATAGACCTTGCATCTCGGCTTCTTCAATATTC
                                                             TIGTGTACTGGCAGAGCTTCTTTGGCCAGCCGTTATTTCCAGGAGAAATTCAGTTGA
                                                                                                                                      TCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCGTGAAAATTCGATGTAT
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The Institute for Genomic Research
The Institute for Genomic Research
9712 Medical Center for Rockville, MD 20850, USA
Email potacto-array@tigr.org
Clones can be requested from the University of Arizona
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:4100"
                                                                                                                                                                                                                                                                                                                                                                    1086 ACCAAGTCTACGCTGCACTGCGCTCGAAGCATGTG 1120
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS91ZE05 of Adult vegetative tissue of strain col-0 of Axabidopsis thaliana (thale cress).
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                                                                                                                                                                                                                                                                                     284 TGGCTGAGCGGGTTGTTGGAACAGGTTCATTCGGGATTGTTTTTCAGGCGAAATGCTTGG
                                                                                                                                                                                                                                                                                                                    136 TGGCTGAACGTGTCGTGGGGACTGGATCATTTGGAGTTGTTTTTCAGGCAAAATGCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               884 TTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAA
                                                                                              164 TGGATTCTGATAAGGAAATGTCTGCAGCTGTTATTGAGGGAAATGACGCTGTTACTGGTC
                                                                                                                                                                                                                 344 AAACTGGAGAATCAGTAGCCATTAAAAAGGTCTTGCAAGATCGACGCTATAAAAACCGTG
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                                                Gaps
                                                ö
  Length 910
                                           Indels
                                              0; Mismatches 200;
  DB 7;
Score 575;
Pred. No. 1
Query Match
Best Local Similarity 77.7%;
Matches 695; Conservative
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743 651 803 711 863 771

591

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591 bp mRNA linear EST 01-APR-2002 mRNA sequence. Arabidopsis thaliana cDNA clone RAFL09-84-D20 S', AV831097
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases I to 591)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
and Shinozaki,K.
                                                                                                                                                                                                                                                                                                      GGTTTTGGAAGTGCAAAGTATTGGTAAAAGGAGAACCAAACATTTCCTACATCTGCTCG 923
                                                                                                                      TACACATATCAAATCTTTAGAGGTTTGGCTTACATCCATACTGTTCCCGGTGTTTGCCCAC
                                                                                                                                                                                                                                                                     GATTTTGGAAGTGCAAAAGTATTGGTCAAAGGTGAACCAAACATATCATATATCTGCTCC
       624 ACTGAAAAAGATGAGCTTTACCTCAATCTTGTTCTTGAGTACGTTCCAGAAACTGTTCAT
                                                                 924 AGGTATTACAGAGCACCTGAACTCATCTTTGGAGCAACCGAGTATACGACACGCATTGAT
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                                            CGGGTTTTGAGGCACTATACTAGTTCTAATCAGAGGATGCCAATTTTCTATGTCAAGCTT
                                                                                                                                                                                           652 AGAGATGTGAAAACCACAAAATCTCTTGGTTGATCCCTTGACCCATCAGGTTAAGCTGTGT
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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

Direct Submission

By 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Welssenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
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Location/Qualifiers
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Pred. No. 3.8e-138;
0; Mismatches 315; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="Adult vegetative tissue"
/plasmid="pcWxspoRT 6"
complement(1. .1638)
/gene="At5g26751"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3702"
/clone="GSLTLS91ZE05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.6%;
                                                                                                                                                                                                                                                                                    (bases 1 to 1638)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          776; Conservative
                                                                                                                                                                                                                                                                 Unpublished
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Matches 776; Conserv
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/dev stage="Pre-bloom"
/lab_host="Disalpha"
/clone_lib="Cabernet Sauvignon Flower Pre-bloom - CABI"
/clone_lib="Cabernet Sauvignon Flower pont, Site_1:
Sfil; Site_2: Sfil; CABI is a cDNA library of Vitis
vinifera cv. 'Cabernet Sauvignon' Clone & flowers. Samples
were collected approximately eleven days before onset of
bloom (clusters at this stage were fully developed and
flowers with calyptras or caps still attached. Sampled
vines were located at the University of California, Davis,
Experimental Vineyard. cDNAs were made by oligo-dT priming
and directionally cloned. 5'and 3' adaptors were used in
                                                                                                                    EST 30-APR-2003
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                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
1 (bases 1 to 829)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J., Jones,K. and Cook,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 TGCAAGATCGACGCTATAAAAACCGTGAGTTGCAACTAATGCGACCAATGGATCACCCAA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 recaggacagaagararaagaarcergagcrecagrraargegeacgargaarcarceaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           437 ATGICAICTCCTTGAAGCACTGTTTCTTCTTCTACAACGAGTAGAGATGAGCTCTTCCTCA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                 CB971865 LIIA_FA HOS Cabernet Sauvignon Flower Pre-bloom - CABI Vitis vinifera cDNA clone CABI0006_IIIa_FA_HOS 5', mRNA seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5'-AAGCAGTGGTATCAACGCAGAGTCGCCATTACGGCCGGG-3' and 5'-ATTCTACAGGCCGACGAGCCGACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and
                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 GGATTGTTTTCAGGCGAAATGCTTGGAAACTGGAGAATCAGTAGCCATTAAAAAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGATTGTTTTCAGGCAAAATGCTTGGAAACTGGAGAGCTGTGGCCATAAAGAAGGTTT
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  542 GCTTTACACATATCAAATCCTTTAAAGGTTTGGCTTACATTCATACTGTT 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.4%; Score 572; DB 6; Length 82 ilarity 80.6%; Pred. No. 1.1e-137; Conservative 0; Mismatches 161; Indels
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/organism="Vitis vinifera"
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/culTivar="Cabernet Sauvignon"
/db xref="texan:29760"
/clone="CAB10006 IIIa_Fa_H05"
/sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Douglas Cook, PhD
CABS Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: ACGGTACCGGACATATGCC. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cloning as follows:
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EST.
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Vitis vinifera
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                                                                                                                                                                                       An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sall. submitted for publication) digested with BamHI and Sall. size (Inttp://www.gsc.riken.go.jp/e/plant/index_e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAGAATCAGTAGCCATTAAAAAGGTCTTGCAAGATCGACGCTATAAAAACCGTGAGTT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTGATAAGGAAATGTCTGCAGCTGTTATTGAGGGAAATGACGCTGTTACTGGTCATAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATTICCACTACTATAGGAGGCAAAAACGGCGAACCAAAGCAGACCATTAGTTACATGGC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAGCGGGTTGTTGGAACAGGTTCATTCGGGATTGTTTTCAGGCGAAATGCTTGGAAAC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAGAATCAGTAGCCATTAAAAAGGTCTTGCAAGATCGACGCTATAAAAACCGTGAGTT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAACTAATGCGACCAATGGATCACCCAAATGTCATCTCCTTGAAGCACTGTTTCTTCTC 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATACCGGGTTTTGAGGCACTATACTAGTTCTAATCAGAGGATGCCAATTTTCTATGTCAA 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTGCTCCGCCGCTGCAGCTTCACGACGCGACGCTTTGAAACGCCGTCCTGAATTGGA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTGCTCCGCCGCTGCAGCTTCACGACGCCGATTGAAACGCCGTCCTGAATTGGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TICTGATAAGGAAATGTCTGCAGCTGTTATTGAGGGAAATGACGCTGTTACTGGTCATAT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/db_xref="taxon:3702"
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/clone="RAFL09-84-D20"
/clone to mature seeds"
/lab_host="DH10B"
/clone lib="RAFL9"
/note="Site_1: BamH1; Site_2: Sal1; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, hr) treatments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGAGAGAAAAGAGTAAAAAAGCACATGGCCTCATTACCATTGGGGCCTCAGCCTCATGC
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  scale analysis of Arabidopsis full-length cDNA (2002b)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                               Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.5%; Score 572.2; DB 1;
99.2%; Pred. No. 8.9e-138;
live 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Arabidopsis thaliana"
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1000 GAAAGCGGTGTTGATCAGCTTGTTGAAATCATCAAGGTTCTGGGCACACCCCACACGTGAA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 GTGACCAGCATTGATGGGAGAAATGGGCAGGCAAAGCAGACCATTAGTTACATGGCTGAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412 CTAATGCGACCAATGGATCACCCAAATGTCATCTCCTTGAAGCACTGTTTCTTCTCTACA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGAGTAGAGATGAGCTCTTCCTCAACCTTGTTATGGAGTATGTACCTGAGACTTTATAC 531
                                                                                                                                                                                                    /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGGTGGTAGGTCATGGGTCCTTCGGAACCGTTTTCCAGGCCAAGTGTCTTGAAACTGGT
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                                                                     /organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:636234"
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/clone lib="Maize Mapping Project/DuPont Cornsensus
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Schnable, Iowa State, then clones may be requested from www.zmdb.iastate.edu.
Location/Qualifiers
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clade, Panicoideae, Andropogoneae, Zea.
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If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat
                     181 ACTTGGTAATGGAATATGTCCCTGAGACTATGGGTCTTGAAGCACTACAGCAATG
                                                                                                                                                                                                                                                                   TAGTTGATCCACTTACTCACCAAGTTAAGCTTTGTGACTTTGGAAAGTGCAAAAGTGCTAG
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                                                                                CTAATCAGAGGATGCCAATTTTCTATGTCAAGCTTTACACATATCAAATCTTTAGAGGTT
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Arthur,L.W. Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design overgo Probes
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952 GAAATTCGATGTATGAACCCGAACTACACAGATTTTAGGTTCCCACAAATCAAAGCTCAC 1011	1060 GAAATTAAGTGCATGAATTATACCGAGTTTAAATTCCCGCAAATCAAAGCTCAC 1119	1012 CCTIGGCACAAGGTTTTCATAAACGGATGCCTCCAGAAGCAATAGACCTTGCATCTCGG 1071	1120 CCATGGCATAAGATATTCCATAAAAGGATGCCTGCTGAGCGGTAGATCTCGTGTCCAGG 1179	1072 CTTCTTCAATATTCACCAAGTCTACGCTGCACTCGAAGCATGTGCTCTGTT 1131	1180 CITCTGCAGTACTCACCAAAACTTCGGTCGGTCGCTTTGGAAGCATTGGTCGTCCGTTC 1239	1132 TTCAATGAACTCCGAGAGCCAAACGCCGTCTTCCAAATGGTCGTCCATTACCGCCATTG 1191	1240 TITGAIGAACTTCGGGATCCAAACACCCGCTTACCGAATGGTCGTTTTCTTCCGCCTCTC 1299	1192 TTCAATTTCAAAC 1204	1300 TTCAATTTTAAGC 1312
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